

ccccccccc	ACACCCCAA	TCCCCACCC	GGCGATCCA	ACCCGAGCACC	TCCCCACCC	360
CCCCAAACG	CACCGCCGC	ACccTTCATT	CCCTCAACG	CACTTACCC	TCTCCGGGTC	360
GACAAACCCG	TTGGAGGATT	CACTTTCGG	CTGCCCTGCG	CTTGTGCTGA	GTCTTGACCC	420
CCCGACTTCG	ACTACGGTTG	ACGACTCTC	AGCAAAACCA	CCGGGGACCC	CCCATTTCCC	480
CCACAGGCGC	CCCGGGTGC	CAATGACACC	CTTATGTCG	TGGGGGCT	AGACGAAAG	540
CTTTACGCGA	GGCTGAAAGC	CACTTACCC	AAGGCCCCCG	CCCGGGTTGG	CTGGGACATG	600
CTTAACTTCT	ATATGCGTA	ACCCGACCC	CGATGACCC	AGGAAACCT	CTGGCTGAC	660
CCCAACGGCG	TCTCTGGAG	ACCTTGTAT	TACCAACTA	AGTTGAGGAA	TCCGACTTAC	720
CCCAACGGCG	AGATCTGGAC	ACGCTTATC	GGCTGGCCG	CCGGGACCC	ACGGGACCC	780
CCGGGGGCTC	AGggCTGGTT	TGGGGGTTG	CTGGGAGCTG	CCGACGACCC	GGTGGACAAAG	840
CCGGGGGCTC	AGGGGGCTAC	CGGATGATC	CGGGGTTGG	TCCGGGGCTC	CCGGGGCCCG	900
CCGGGGGCTC	CTGGAGGAGC	CGCTGGCG	CCGGGGCCCG	CCGGGGAACT	CGCTCTTAC	960
CCGGGGGCTC	CGACACCCG	CCGGACCTTA	CCGGGGCTCA			999

(II) INFORMATION FOR SEQ ID NO:51:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met	His	His	His	His	His	Met	His	Gln	Val	Asp	Pro	Asn	Ieu	Thr		
2						5			10				15			
Arg	Arg	Lys	Gly	Arg	Ieu	Ala	Ala	Ieu	Ala	Ile	Ala	Met	Ala	Ser		
20						25			30				35			
Ala	Ser	Ieu	Val	Thr	Val	Ala	Val	Pro	Ala	Thr	Ala	Asn	Ala	Asp	Pro	
35						40				45					50	
Glu	Pro	Ala	Pro	Pro	Val	Pro	Thr	Thr	Ala	Ala	Ser	Pro	Pro	Ser	Thr	
55					55				60						65	
Ala	Ala	Ala	Pro	Pro	Ala	Pro	Ala	Thr	Pro	Val	Ala	Pro	Pro	Pro	Pro	
65					70				75						80	
Ala	Ala	Ala	Asn	Thr	Pro	Asn	Ala	Gln	Pro	Gly	Asp	Pro	Asn	Ala	Ala	
85					90				95						100	
Pro	Pro	Pro	Ala	Asp	Pro	Asn	Ala	Pro	Pro	Pro	Pro	Pro	Val	Ile	Ala	Pro

100	108	116	
Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser			
115	120	125	
Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp			
130	135	140	
Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro			
145	150	155	160
Gly Glu Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg			
165	170	175	
Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala			
180	185	190	
Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro			
195	200	205	
Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val			
210	215	220	
Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys			
225	230	235	240
Pro Asn Gly Ile Try Thr Gly Val Ile Gly Ser Pro Ala Ala Asn			
245	250	255	
Ala Pro Asp Ala Gly Pro Pro Glu Arg Try Phe Val Val Trp Leu Gly			
260	265	270	
Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu			
275	280	285	
Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro			
290	295	300	
Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr			
305	310	315	320
Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala			
325	330		

(C) INFORMATION FOR SEQ ID NO:64:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Asp Pro Val Asp Ala Val Ile Asn Thr Thr Lys Asn Tyr Gly Glu Val

1	5	10	15
Val	Ala	Ala	Leu
	20		

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala	Val	Glu	Ser	Gly	Met	Leu	Ala	Leu	Gly	Thr	Pro	Ala	Pro	Ser
1	5						10						15	

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala	Ala	Met	Lys	Pro	Arg	Thr	Gly	Asp	Gly	Pro	Leu	Glu	Ala	Ala	Lys
1	5						10					15			
		Glu	Gly	Arg											

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr	Tyr	Trp	Cys	Pro	Gly	Gln	Pro	Phe	Asp	Pro	Ala	Trp	Gly	Pro
1	5						10					15		

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Asp Ile Gly Ser Glu Ser Thr Ala Asp Gln Gln Xaa Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Ala Ala Ala Ala Pro Pro
1 5 10 15

Ala

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ala Pro Lys Thr Tyr Xaa Glu Glu Leu Lys Gly Thr Asp Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53.

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Gln Thr Ser
1 8 16 25

Leu Leu Asn Asn Leu Ala Asp Pro Asp Val Ser Ser Phe Ala Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:63:

1.1 SEQUENCE CHARACTERISTICS

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

Gly Cys Gly Asp Arg Ser Gly Gly Asn Leu Asp Glu Ile Arg Lys Arg
 1 5 10 15

Arg Asp Arg Ser Gly Gly Asn Leu
20

(2) INFORMATION FOR SEQ ID NO:64:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(END) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Thr Gly Ser Leu Asn Glu Thr His Asn Arg Arg Arg Ala Asn Glu Arg Iys
 1 5 10 15 20 25

Aaa Thr Thr Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala
20 30

Ala Ala Ala Ile Gly Ala Ala Ala Ala Gly Val Thr Ser Ile Met Ala
38 48 48

Gly Gly Pro Val Val Tyr Glu Met Gln Pro Val Val Phe Gly Ala Pro
 ⁵⁰ ⁵⁵ ⁶⁰

Leu Pro Leu Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Glu
65 70 75 80 85

Leu Thr Ser Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser The Ala
as as as as

Asn Lys Gly Ser Ile Val Glu Gly Gly Ile Gly Gly Thr Glu Ala Arg
100 105 110

Ile	Ala	Asp	His	Lys	Leu	Lys	Lys	Ala	Ala	Glu	His	Gly	Asp	Leu	Pro
115								120						125	
Leu	Ser	Phe	Ser	Val	Thr	Asn	Ile	Gln	Pro	Ala	Ala	Ala	Gly	Ser	Ala
130							135						140		
Thr	Ala	Asp	Val	Ser	Val	Ser	Gly	Pro	Lys	Leu	Ser	Ser	Pro	Val	Thr
145							150						155		160
Gln	Asn	Val	Thr	Phe	Val	Asn	Gln	Gly	Gly	Trp	Met	Leu	Ser	Arg	Ala
165							170						175		
Ser	Ala	Met	Glu	Leu	Leu	Gln	Ala	Ala	Gly	Xaa					
180							185								

(2) INFORMATION FOR SEQ ID NO: 35.

(4) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANGENESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

Asp Glu Val Thr Val Glu Thr Thr Ser Val Phe Arg Ala Asp Phe Leu
 1 S 40 50

Ser Glu Leu Asp Ala Pro Ala Gin Ala Gly Thr Glu Ser Ala Val Ser
30 30 30

Gly Val Glu Gly Ieu Pro Pro Gly Ser Ala Ieu Ieu Val Val Lys Arg
35 40 45

Gly Pro Asn Ala Gly Ser Arg Phe Leu Leu Asp Gln Ala Ile Thr Ser
asparagine serine

Ala Gly Arg His Pro Asp Ser Asp Ile Phe Leu Asp Asp Val Thr Val
55 56 57 58 59 60 61 62 63 64 65 66

Ser Arg Arg His Ala Glu Phe Arg Leu Glu Asn Asn Glu Phe Asn Val
33 34 35 36 37 38 39 40 41 42 43 44

Val Asp Val Gly Ser Leu Asn Gly Thr Tyr Val Asn Arg Glu Pro Val

Asp Ser Ala Val Leu Ala Asn Gly Asp Glu Val Gln Ile Gly Lys Leu

Arg Leu Val Phe Leu Thr Gly Pro Lys Gln Gly Glu Asp Asp Gly Ser

The Gly-Gly-Pro Sequence

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Thr Ser Asn Arg Pro Ala Arg Arg Gly Arg Arg Ala Pro Arg Asp Thr				
1	5	10	15	
Gly Pro Asp Arg Ser Ala Ser Leu Ser Leu Val Arg His Arg Arg Gln				
20	25	30	35	
Gln Arg Asp Ala Leu Cys Leu Ser Ser Thr Gln Ile Ser Arg Gln Ser				
35	40	45	50	
Asn Leu Pro Pro Ala Ala Gly Gly Ala Ala Asn Tyr Ser Arg Arg Asn				
55	60	65	70	
Phe Asp Val Arg Ile Lys Ile Phe Met Leu Val Thr Ala Val Val Leu				
65	70	75	80	
Leu Cys Cys Ser Gly Val Ala Thr Ala Ala Pro Lys Thr Tyr Cys Glu				
85	90	95	100	
Glu Leu Lys Cys Thr Asp Thr Cys Gln Ala Cys Gln Ile Gln Met Ser				
105	110	115	120	
Asp Pro Ala Tyr Asn Ile Asn Ile Ser Leu Pro Ser Tyr Tyr Pro Asp				
115	120	125	130	
Gln Lys Ser Leu Glu Asn Tyr Ile Ala Gln Thr Arg Asp Lys Phe Leu				
135	140	145	150	
Ser Ala Ala Thr Ser Ser Thr Pro Arg Gln Ala Pro Tyr Glu Leu Asn				
145	150	155	160	
Ile Thr Ser Ala Thr Tyr Gln Ser Ala Ile Pro Pro Arg Gly Thr Gln				
165	170	175	180	
Ala Val Val Leu Ile Val Tyr His Asn Ala Gly Cys Thr His Pro Thr				
180	185	190	195	
Thr Thr Tyr Lys Ala Phe Asp Trp Asp Gln Ala Tyr Arg Lys Pro Ile				
195	200	205	210	
Thr Tyr Asp Thr Leu Trp Gln Ala Asp Thr Asp Pro Leu Pro Val Val				
210	215	220	225	
Phe Pro Ile Val Ala Arg				
225	230			

(2) INFORMATION FOR SEQ ID NO:67:

(ii) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1 5 10 15

Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
20 28 36 38

Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
as as as as

Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Glu Arg Val
SC SSS SC

Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
 85 78 78 80

Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
85 86 87

Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
100 108 110

Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Ieu Ala Glu
118 129 130

Gly Pro Pro Ala
330

(2) INFORMATION FOR EEC ID NO.: 68:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANGENESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

Val Pro Leu Arg Ser Pro Ser Met Ser Pro Ser Lys Cys Leu Ala Ala
1 5 10 15

Ala Gln Arg Asn Pro Val Ile Arg Arg Arg Arg Lys Ser Asn Pro Pro
30 35 40

Pro Arg Lys Tyr Arg Ser Met Pro Ser Pro Ala Thr Ala Ser Ala Gly
38 40 42

Met Ala Arg Val Arg Arg Arg Ala Ile Trp Arg Gly Pro Ala Thr Xaa
 50 55 60

Ser Ala Gly Met Ala Arg Val Arg Arg Trp Xaa Val Met Pro Xaa Val
 65 70 75 80

Ile Gln Ser Thr Xaa Ile Arg Xaa Xaa Gly Pro Phe Asp Asn Arg Gly
 85 90 95

Ser Glu Arg Lys
 100

(3) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Thr Asp Asp Ile Leu Leu Ile Asp Thr Asp Glu Arg Val Arg Thr
 1 8 10 18

Leu Thr Leu Asn Arg Pro Gln Ser Arg Asn Ala Leu Ser Ala Ala Leu
 20 25 30

Arg Asp Arg Phe Phe Ala Xaa Leu Xaa Asp Ala Glu Xaa Asp Asp Asp
 35 40 45

Ile Asp Val Val Ile Leu Thr Gly Ala Asp Pro Val Phe Cys Ala Gly
 50 55 60

Leu Asp Leu Lys Val Ala Gly Arg Ala Asp Arg Ala Ala Gly Xaa Leu
 65 70 75 80

Thr Ala Val Gly Gly His Asp Gln Ala Gly Asp Arg Arg Asp Gln Arg
 85 90 95

Arg Arg Gly His Arg Arg Ala Arg Thr Gly Ala Val Leu Arg His Pro
 100 105 110

Asp Arg Leu Arg Ala Arg Pro Leu Arg Arg His Pro Arg Pro Gly Gly
 115 120 125

Ala Ala Ala His Leu Gly Thr Gln Cys Val Leu Ala Ala Lys Gly Arg
 130 135 140

His Arg Xaa Gly Pro Val Asp Glu Pro Asp Arg Arg Leu Pro Val Arg
 145 150 155 160

Asp Arg Arg

(2) INFORMATION FOR USE IN NO. 70:

III. SEQUENCE CHARACTERISTICS

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met	Lys	Phe	Val	Asn	His	Ile	Glu	Pro	Val	Ala	Pro	Arg	Arg	Ala	Gly
1				5					10					15	
Gly	Ala	Val	Ala	Glu	Val	Tyr	Ala	Glu	Ala	Arg	Arg	Glu	Phe	Gly	Arg
				20				25					30		
Leu	Pro	Glu	Pro	Leu	Ala	Met	Leu	Ser	Pro	Asp	Glu	Gly	Leu	Leu	Thr
				35				40					45		
Ala	Gly	Trp	Ala	Thr	Leu	Arg	Glu	Thr	Leu	Leu	Val	Gly	Gly	Val	Pro
				50			55				60				
Arg	Gly	Arg	Lys	Glu	Ala	Val	Ala	Ala	Val	Ala	Ala	Ser	Leu	Arg	
			65			70			75				80		
Cys	Pro	Trp	Cys	Val	Asp	Ala	His	Thr	Met	Leu	Tyr	Ala	Ala	Gly	
				85			90			95			100		
Gln	Thr	Asp	Thr	Ala	Ala	Ala	Ile	Leu	Ala	Gly	Thr	Ala	Pro	Ala	Ala
				105			110			115			120		
Gly	Asp	Pro	Asn	Ala	Pro	Tyr	Val	Ala	Trp	Ala	Ala	Gly	Thr	Gly	Thr
				125			130			135			140		
Pro	Ala	Gly	Pro	Pro	Ala	Pro	Phe	Gly	Pro	Asp	Val	Ala	Ala	Gly	Tyr
				145			150			155			160		
Leu	Gly	Thr	Ala	Val	Gln	Phe	His	Phe	Ile	Ala	Arg	Leu	Val	Leu	Val
				165			170			175			180		
Leu	Leu	Asp	Glu	Thr	Phe	Leu	Pro	Gly	Gly	Pro	Arg	Ala	Gln	Gly	Leu
				185			190			195			200		
Met	Arg	Arg	Ala	Gly	Gly	Leu	Val	Phe	Ala	Arg	Lys	Val	Arg	Ala	Glu
				205			210			215			220		
His	Arg	Pro	Gly	Arg	Ser	Thr	Arg	Arg	Leu	Glu	Pro	Arg	Thr	Leu	Pro
				225			230			235			240		
Asp	Asp	Leu	Ala	Trp	Ala	Thr	Pro	Ser	Glu	Pro	Ile	Ala	Thr	Ala	Phe
				245			250			255			260		
Ala	Ala	Leu	Ser	His	His	Leu	Asp	Thr	Ala	Pro	His	Leu	Pro	Pro	Pro
				265			270			275			280		

Thr Arg Gln Val Val Arg Arg Val Val Gly Ser Trp His Gly Glu Pro
 345 256 255
 Met Pro Met Ser Ser Arg Trp Thr Asn Glu His Thr Ala Glu Leu Pro
 260 265 270
 Ala Asp Leu His Ala Pro Thr Arg Leu Ala Leu Leu Thr Gly Ile Ala
 275 280 285
 Pro His Gln Val Thr Asp Asp Asp Val Ala Ala Ala Arg Ser Leu Leu
 290 295 300
 Asp Thr Asp Ala Ala Leu Val Gly Ala Leu Ala Trp Ala Ala Phe Thr
 305 310 315 320
 Ala Ala Arg Arg Ile Gly Thr Trp Ile Gly Ala Ala Ala Glu Gly Gln
 325 330 335
 Val Ser Arg Gln Asn Pro Thr Gly
 340

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Asp Asp Pro Asp Met Pro Gly Thr Val Ala Lys Ala Val Ala Asp Ala
 1 5 10 15
 Leu Gly Arg Gly Ile Ala Pro Val Glu Asp Ile Gln Asp Cys Val Glu
 20 25 30
 Ala Arg Leu Gly Glu Ala Gly Leu Asp Asp Val Ala Arg Val Tyr Ile
 35 40 45
 Ile Tyr Arg Gln Arg Arg Ala Glu Leu Arg Thr Ala Lys Ala Leu Leu
 50 55 60
 Gly Val Arg Asp Glu Leu Lys Leu Ser Leu Ala Ala Val Thr Val Leu
 65 70 75 80
 Arg Glu Arg Tyr Leu Leu His Asp Glu Gln Gly Arg Pro Ala Glu Ser
 85 90 95
 Thr Gly Glu Leu Met Asp Arg Ser Ala Arg Cys Val Ala Ala Glu
 100 105 110
 Asp Gln Tyr Glu Pro Gly Ser Ser Arg Arg Trp Ala Glu Arg Phe Ala
 115 120 125

Thr Leu Leu Arg Asn Leu Glu Phe Leu Pro Asn Ser Pro Thr Leu Met
 130 135 140
 Asn Ser Gly Thr Asp Leu Gly Leu Leu Ala Gly Cys Phe Val Leu Pro
 145 150 155 160
 Ile Glu Asp Ser Leu Gln Ser Ile Phe Ala Thr Leu Gly Gln Ala Ala
 165 170 175
 Glu Leu Gln Arg Ala Gly Gly Thr Gly Tyr Ala Phe Ser His Leu
 180 185 190
 Arg Pro Ala Gly Asp Arg Val Ala Ser Thr Gly Gly Thr Ala Ser Gly
 195 200 205
 Pro Val Ser Phe Leu Arg Leu Tyr Asp Ser Ala Ala Gly Val Val Ser
 210 215 220
 Met Gly Gly Arg Arg Arg Gly Ala Cys Met Ala Val Leu Asp Val Ser
 225 230 235 240
 His Pro Asp Ile Cys Asp Phe Val Thr Ala Lys Ala Glu Ser Pro Ser
 245 250 255 260
 Glu Leu Pro His Phe Asn Leu Ser Val Gly Val Thr Asp Ala Phe Leu
 265 270
 Arg Ala Val Glu Arg Asn Gly Leu His Arg Leu Val Asn Pro Arg Thr
 275 280 285
 Gly Lys Ile Val Ala Arg Met Pro Ala Ala Glu Leu Phe Asp Ala Ile
 290 295 300
 Cys Lys Ala Ala His Ala Gly Gly Asp Pro Gly Leu Val Phe Leu Asp
 305 310 315 320
 Thr Ile Asn Arg Ala Asn Pro Val Pro Gly Arg Gly Arg Ile Glu Ala
 325 330 335
 Thr Asn Pro Cys Gly Glu Val Pro Leu Leu Pro Tyr Glu Ser Cys Asn
 340 345 350
 Leu Gly Ser Ile Asn Leu Ala Arg Met Leu Ala Asp Gly Arg Val Asp
 355 360 365
 Trp Asp Arg Leu Glu Glu Val Ala Gly Val Ala Val Arg Phe Leu Asp
 370 375 380
 Asp Val Ile Asp Val Ser Arg Tyr Pro Phe Pro Glu Leu Gly Glu Ala
 385 390 395 400
 Ala Arg Ala Thr Arg Lys Ile Gly Leu Gly Val Met Gly Leu Ala Glu
 405 410 415

Leu Leu Ala Ala Leu Gly Ile Pro Tyr Asp Ser Glu Glu Ala Val Arg
 420 425 430

Leu Ala Thr Arg Leu Met Arg Arg Ile Glu Glu Ala Ala His Thr Ala
 435 440 445

Ser Arg Arg Leu Ala Glu Glu Arg Gly Ala Phe Pro Ala Phe Thr Asp
 450 455 460

Ser Arg Phe Ala Arg Ser Gly Pro Arg Arg Asn Ala Gln Val Thr Ser
 465 470 475 480

Val Ala Pro Thr Gly
 485

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Gly Val Ile Val Leu Asp Leu Glu Pro Arg Gly Pro Leu Pro Thr Glu
 1 5 10 15

Ile Tyr Trp Arg Arg Arg Gly Leu Ala Leu Gly Ile Ala Val Val Val
 20 25 30

Val Gly Ile Ala Val Ala Ile Val Ile Ala Phe Val Asp Ser Ser Ala
 35 40 45

Gly Ala Lys Pro Val Ser Ala Asp Lys Pro Ala Ser Ala Gln Ser His
 50 55 60

Pro Gly Ser Pro Ala Pro Glu Ala Pro Glu Pro Ala Gly Glu Thr Glu
 65 70 75 80

Gly Asn Ala Ala Ala Ala Pro Pro Glu Gly Glu Asn Pro Glu Thr Pro
 85 90 95

Thr Pro Thr Ala Ala Val Glu Pro Pro Val Leu Lys Glu Gly Asp
 100 105 110

Asp Cys Pro Asp Ser Thr Leu Ala Val Lys Gly Leu Thr Asn Ala Pro
 115 120 125

Gln Tyr Tyr Val Gly Asp Glu Pro Lys Phe Thr Met Val Val Thr Asn
 130 135 140

Ile Gly Leu Val Ser Cys Lys Arg Asp Val Gly Ala Ala Val Leu Ala
 145 150 155 160

Ala	Tyr	Val	Tyr	Ser	Ieu	Asp	Asn	Lys	Arg	Ieu	Trp	Ser	Asn	Ieu	Asp
					163					170					175
Cys	Ala	Pro	Ser	Asn	Glu	Thr	Ieu	Val	Lys	Thr	Phe	Ser	Pro	Gly	Glu
					180					185					190
Gln	Val	Thr	Thr	Ala	Val	Thr	Trp	Thr	Gly	Met	Gly	Ser	Ala	Pro	Arg
					195					200					205
Cys	Pro	Ieu	Pro	Arg	Pro	Ala	Ile	Gly	Pro	Gly	Thr	Tyr	Asn	Ieu	Val
					210					215					220
Val	Gln	Ieu	Gly	Asn	Ieu	Arg	Ser	Ieu	Pro	Val	Pro	Phe	Ile	Ieu	Asn
					225					230			235		240
Gln	Pro	Pro	Pro	Pro	Gly	Pro	Val	Pro	Ala	Pro	Gly	Pro	Ala	Gln	
					245					250					255
Ala	Pro	Pro	Pro	Glu	Ser	Pro	Ala	Gln	Gly	Gly					
					260					265					

(3) INFORMATION FOR GPO ID NO: 733

SCIENCE CHARACTERISTICS

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANGENESS: single
- (D) TOPOLOGY: linear

(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

(2) INFORMATION FOR SEQ ID NO: 740

3.1 SEQUENCE CHARACTERISTICS

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1a

Cys Gly Gly Gly Thr Asn Ser Ser Ser Ser Gly Ala Gly Gly Thr Ser
 28 31 34 37 40 43 46 49 52 55 58 61 64 67 70 73 76

Gly Ser Val His Cys Gly Gly Lys Lys Glu Leu His Ser Ser Gly Ser
 35 40 45

Thr Ala Glu Glu Asn Ala Met Glu Gln Phe Val Tyr Ala Tyr Val Arg
35 36 37 38 39 40 41 42 43 44 45 46 47 48

Ser Cys Pro Gly Tyr Thr Leu Asp Tyr Asn Ala Asn Gly Ser Gly Ala
65 70 75 80

Gly Val Thr Glu Phe Leu Asn Asn Glu Thr Asp Phe Ala Gly Ser Asp
ss ss ss

Val Pro Leu Asn Pro Ser Thr Gly Glu Pro Asp Arg Ser Ala Glu Arg
100 108 110

Cys Gly Ser Pro Ala Trp Asp Leu Pro Thr Val Ile Gly Pro Ile Ala
115 . . 120 . . 125

Ile Thr Tyr Asn Ile Lys Gly Val Ser Thr Leu Asn Leu Asp Gly Pro
120 121 122 123 124 125

The His Lys Ile She Asn Gly Thr Ile Thr Val Trp Asn Asp Pro

Gln Ile Gln Ala Leu Asn Ser Gly Thr Asp Leu Pro Pro Thr Pro Ile
188 189 190 191 192 193 194 195 196 197 198

Ser Val Ile Phe Arg Ser Asp Lys Ser Gly Thr Ser Asp Asn Phe Gln
 180 181 182 183 184 185 186 187 188 189 190

Lys Tyr Leu Asp Gly Val Ser Asn Gly Ala Trp Gly Lys Gly Ala Ser
100 200 300

Glu Thr Phe Ser Gly Gly Val Gly Val Gly Ala Ser Gly Asn Asn Gly
310 315 320

Thr Ser Ala Leu Leu Glu Thr Thr Asp Gly Ser Ile Thr Tyr Asp Glu
328 329 330 331 332 333 334 335 336 337

Trp Ser Phe Ala Val Gly Lys Glu Leu Asn Met Ala Gln Ile Ile Thr
225 230 235 240 245

Ser Ala Gly Pro Asp Pro Val Ala Ile Thr Thr Glu Ser Val Gly Lys
 260 265 270

Thr Ile Ala Gly Ala Lys Ile Met Gly Gln Gly Asn Asp Leu Val Leu
 275 280 285

Asp Thr Ser Ser Phe Tyr Arg Pro Thr Gln Pro Gly Ser Tyr Pro Ile
 290 295 300

Val Leu Ala Thr Tyr Glu Ile Val Cys Ser Lys Tyr Pro Asp Ala Thr
 305 310 315 320

Thr Gly Thr Ala Val Arg Ala Phe Met Gln Ala Ala Ile Gly Pro Gly
 325 330 335

Gln Glu Gly Leu Asp Gln Tyr Gly Ser Ile Pro Leu Pro Lys Ser Phe
 340 345 350

Gln Ala Lys Leu Ala Ala Ala Val Asn Ala Ile Ser
 355 360

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Gln Ala Ala Ala Gly Arg Ala Val Arg Arg Thr Gly His Ala Glu Asp
 1 5 10 15

Gln Thr His Gln Asp Arg Leu His His Gly Cys Arg Arg Ala Ala Val
 20 25 30

Val Val Arg Gln Asp Arg Ala Ser Val Ser Ala Thr Ser Ala Arg Pro
 35 40 45

Pro Arg Arg His Pro Ala Gln Gly His Arg Arg Arg Val Ala Pro Ser
 50 55 60

Gly Gly Arg Arg Arg Pro His Pro His His Val Gln Pro Asp Asp Arg
 65 70 75 80

Arg Asp Arg Pro Ala Leu Leu Asp Arg Thr Gln Pro Ala Glu His Pro
 85 90 95

Asp Pro His Arg Arg Gly Pro Ala Asp Pro Gly Arg Val Arg Gly Arg
 100 105 110

Gly Arg Leu Arg Arg Val Asp Asp Gly Arg Leu Gln Pro Asp Arg Asp
 115 120 125

Ala Asp His Gly Ala Pro Val Arg Gly Arg Gly Pro His Arg Gly Val
 130 135 140
 Gln His Arg Gly Gly Pro Val Phe Val Arg Arg Val Pro Gly Val Arg
 145 150 155 160
 Cys Ala His Arg Arg Gly His Arg Arg Val Ala Ala Pro Gly Gln Gly
 165 170 175
 Asp Val Leu Arg Ala Gly Leu Arg Val Glu Arg Leu Arg Pro Val Ala
 180 185 190
 Ala Val Glu Asn Leu His Arg Gly Ser Gln Arg Ala Asp Gly Arg Val
 195 200 205
 Phe Arg Pro Ile Arg Arg Gly Ala Arg Leu Pro Ala Arg Arg Ser Arg
 210 215 220
 Ala Gly Pro Gln Gly Arg Leu His Leu Asp Gly Ala Gly Pro Ser Pro
 225 230 235 240
 Leu Pro Ala Arg Ala Gly Gln Gln Pro Ser Ser Ala Gly Gly Arg
 245 250 255
 Arg Ala Gly Gly Ala Glu Arg Ala Asp Pro Gly Gln Arg Gly Arg His
 260 265 270
 His Gln Gly Gly His Asp Pro Gly Arg Gln Gly Ala Gln Arg Gly Thr
 275 280 285
 Ala Gly Val Ala His Ala Ala Gly Pro Arg Arg Ala Ala Val Arg
 290 295 300
 Asn Arg Pro Arg Arg
 305

(ii) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ser Ala Val Trp Cys Leu Asn Gly Phe Thr Gly Arg His Arg His Gly
 1 5 10 15
 Arg Cys Arg Val Arg Ala Ser Gly Trp Arg Ser Ser Asn Arg Trp Cys
 20 25 30
 Ser Thr Thr Ala Asp Cys Cys Ala Ser Lys Thr Pro Thr Gln Ala Ala
 35 40 45

Ser Pro Leu Glu Arg Arg Phe Thr Cys Cys Ser Pro Ala Val Gly Cys
 50 55 60

 Arg Phe Arg Ser Phe Pro Val Arg Arg Leu Ala Leu Gly Ala Arg Thr
 65 70 75 80

 Ser Arg Thr Leu Gly Val Arg Arg Thr Leu Ser Glu Trp Asn Leu Ser
 85 90 95

 Pro Arg Ala Glu Pro Ser Cys Ala Val Thr Val Glu Ser His Thr His
 100 105 110

 Ala Ser Pro Arg Met Ala Lys Leu Ala Arg Val Val Gly Leu Val Glu
 115 120 125

 Glu Glu Glu Pro Ser Asp Met Thr Asn His Pro Arg Tyr Ser Pro Pro
 130 135 140

 Pro Glu Glu Pro Gly Thr Pro Gly Tyr Ala Glu Gly Glu Glu Thr
 145 150 155 160

 Tyr Ser Glu Glu Phe Asp Trp Arg Tyr Pro Pro Ser Pro Pro Pro Glu
 165 170 175

 Pro Thr Glu Tyr Arg Glu Pro Tyr Glu Ala Leu Gly Gly Thr Arg Pro
 180 185 190

 Gly Leu Ile Pro Gly Val Ile Pro Thr Met Thr Pro Pro Pro Gly Met
 195 200 205

 Val Arg Glu Arg Pro Arg Ala Gly Met Leu Ala Ile Gly Ala Val Thr
 210 215 220

 Ile Ala Val Val Ser Ala Gly Ile Gly Gly Ala Ala Ala Ser Leu Val
 225 230 235 240

 Gly Phe Asn Arg Ala Pro Ala Gly Pro Ser Gly Gly Pro Val Ala Ala
 245 250 255

 Ser Ala Ala Pro Ser Ile Pro Ala Ala Asn Met Pro Pro Gly Ser Val
 260 265 270

 Glu Glu Val Ala Ala Lys Val Val Pro Ser Val Val Met Leu Glu Thr
 275 280 285

 Asp Leu Gly Arg Glu Ser Glu Glu Gly Ser Gly Ile Ile Leu Ser Ala
 290 295 300

 Glu Gly Leu Ile Leu Thr Asn Asn His Val Ile Ala Ala Ala Lys
 305 310 315 320

 Pro Pro Leu Gly Ser Pro Pro Pro Lys Thr Thr Val Thr Phe Ser Asp
 325 330 335

 Gly Arg Thr Ala Pro Phe Thr Val Val Gly Ala Asp Pro Thr Ser Asp

340	345	350	
Ile Ala Val Val Arg Val Gln Gly Val Ser Gly Leu Thr Pro Ile Ser			
355	360	365	
Leu Gly Ser Ser Ser Asp Leu Arg Val Gly Gln Pro Val Leu Ala Ile			
370	375	380	
Gly Ser Pro Leu Gly Leu Glu Gly Thr Val Thr Thr Gly Ile Val Ser			
385	390	395	400
Ala Leu Asn Arg Pro Val Ser Thr Thr Gly Glu Ala Gly Asn Gln Asn			
405	410	415	
Thr Val Leu Asp Ala Ile Gln Thr Asp Ala Ala Ile Asn Pro Gly Asn			
420	425	430	
Ser Gly Gly Ala Leu Val Asn Met Asn Ala Gln Leu Val Gly Val Asn			
435	440	445	
Ser Ala Ile Ala Thr Leu Gly Ala Asp Ser Ala Asp Ala Gln Ser Gly			
450	455	460	
Ser Ile Gly Leu Gly Phe Ala Ile Pro Val Asp Gln Ala Lys Arg Ile			
465	470	475	480
Ala Asp Gln Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly			
485	490	495	
Val Gln Val Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Gln			
500	505	510	
Val Val Ala Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val			
515	520	525	
Val Val Thr Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu			
530	535	540	
Val Ala Ala Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr			
545	550	555	560
Phe Gln Asp Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly			
565	570	575	
Lys Ala Glu Gln			
580			

(2) INFORMATION FOR SEQ ID NO:77:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met Asn Asp Gly Lys Arg Ala Val Thr Ser Ala Val Leu Val Val Leu
 1 5 10 15

Gly Ala Cys Leu Ala Leu Trp Leu Ser Gly Cys Ser Ser Pro Lys Pro
 20 25 30

Asp Ala Glu Glu Glu Gly Val Pro Val Ser Pro Thr Ala Ser Asp Pro
 35 40 45

Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala Thr Lys Gly Leu
 50 55 60

Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys Val Asp Ser Leu
 65 70 75 80

Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala Asn Pro Leu Ala
 85 90 95

Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Gln Gly Val Pro Phe Arg
 100 105 110

Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp Asp Trp Ser Asn
 115 120 125

Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val Leu Asp Pro Ala
 130 135 140

Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn Leu Gln Ala Gln
 145 150 155 160

Gly Thr Glu Val Ile Asp Gly Ile Ser Thr Thr Lys Ile Thr Gly Thr
 165 170 175

Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly Ala Lys Ser Ala
 180 185 190

Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser His His Leu Val
 195 200 205

Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln Leu Thr Gln Ser
 210 215 220

Lys Trp Asn Glu Pro Val Asn Val Asp
 225 230

(xii) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Val Ile Asp Ile Ile Gly Thr Ser Pro Thr Ser Trp Glu Gln Ala Ala
 1 5 10 15
 Ala Glu Ala Val Glu Arg Ala Arg Asp Ser Val Asp Asp Ile Arg Val
 20 25 30
 Ala Arg Val Ile Glu Glu Asp Met Ala Val Asp Ser Ala Gly Lys Ile
 35 40 45
 Thr Tyr Arg Ile Lys Leu Glu Val Ser Phe Lys Met Arg Pro Ala Glu
 50 55 60
 Pro Arg
 65

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Val Pro Pro Ala Pro Pro Leu Pro Pro Pro Ser Pro Ile Ser
 1 5 10 15
 Cys Ala Ser Pro Pro Ser Pro Pro Leu Pro Pro Ala Pro Pro Val Ala
 20 25 30
 Pro Gly Pro Pro Met Pro Pro Leu Asp Pro Trp Pro Pro Ala Pro Pro
 35 40 45
 Leu Pro Tyr Ser Thr Pro Pro Gly Ala Pro Leu Pro Pro Ser Pro Pro
 50 55 60
 Ser Pro Pro Leu Pro
 65

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Met Ser Asn Ser Ser Arg Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser
 1 5 10 15

Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
 20 28 36

 Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
 35 40 45

 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
 50 56 60

 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 65 70 75 80

 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85 90 95

 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 100 105 110

 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 115 120 125

 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 130 135 140

 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 145 150 155 160

 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 165 170 175

 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Gln Thr
 180 185 190

 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205

 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220

 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 225 230 235 240

 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255

 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270

 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 275 280 285

 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300

 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp

308	310	312	320
Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Thr Gln			
328	330	332	
Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Gln Gly			
340	342	350	
Pro Pro Ala			
388			

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ser Pro Lys Pro Asp Ala Glu Glu Gln Gly Val Pro Val Ser Pro Thr			
1	8	10	18
Ala Ser Asp Pro Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala			
26	28	30	
Thr Lys Gly Leu Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys			
38	40	45	
Val Asp Ser Leu Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala			
56	58	60	
Asn Pro Ile Ala Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Gln Gly			
68	70	75	80
Val Pro Phe Arg Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp			
86	90	95	
Asp Thr Ser Asn Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val			
104	106	110	
Leu Asp Pro Ala Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn			
116	120	128	
Leu Gln Ala Gln Gly Thr Glu Val Ile Asp Gly Ile Ser Thr Thr Lys			
136	138	140	
Ile Thr Gly Thr Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly			
146	150	158	160
Ala Lys Ser Ala Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser			
166	170	176	
Gln His Leu Val Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln			

180	185	190
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Leu Thr Gln Ser Lys Trp Asn Glu Pro Val Asn Val Asp	195	200
	200	205

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val	1	5
	5	10
		15

Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln	20	25
	20	25
		30

His Ala Asp Gly His Ser Leu Leu Asp Ala Thr Asn Pro Ala Val	35	40
	35	40
		45

Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Xaa Glu	50	55
	50	55
		60

Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe	65	70
	65	70
		75
		80

Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Gln Pro Pro Glu Pro Glu	85	90
	85	90
		95

Asn Phe Asp Pro Glu Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala	100	105
	100	105
		110

Ala Thr Glu Gln Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val	115	120
	115	120
		125

Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala Ala Glu Trp	130	135
	130	135
		140

Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn	145	150
	145	150
		155
		160

Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg	165	170
	165	170
		175

Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly	180	185
	180	185
		190

Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Gln Ile	195	200
	195	200
		205

Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe		
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210

215

220

Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp
 225 230 235 240

Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg
 245 250 255 260

Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln
 265 270 275 280

Leu Pro Gly Phe Asp Gln Gly Gly Leu Arg Pro Lys
 275 280 285 290

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Thr Lys Phe His Ala Leu Met Gln Glu Gln Ile His Asn Gln Phe Thr
 1 5 10 15

Ala Ala Gln Gln Tyr Val Ala Ile Ala Val Tyr Phe Asp Ser Glu Asp
 20 25 30

Leu Pro Gln Leu Ala Lys His Phe Tyr Ser Gln Ala Val Glu Glu Arg
 35 40 45

Asn His Ala Met Met Leu Val Gln His Leu Leu Asp Arg Asp Leu Arg
 50 55 60

Val Glu Ile Pro Gly Val Asp Thr Val Arg Asn Gln Phe Asp Arg Pro
 65 70 75 80

Arg Glu Ala Leu Ala Leu Ala Asp Gln Glu Arg Thr Val Thr Asp
 85 90 95

Gln Val Gly Arg Leu Thr Ala Val Ala Arg Asp Glu Gly Asp Phe Leu
 100 105 110

Gly Glu Gln Phe Met Gln Trp Phe Leu Gln Gln Ile Glu Glu Val
 115 120 125

Ala Leu Met Ala Thr Leu Val Arg Val Ala Asp Arg Ala Gly Ala Asn
 130 135 140

Leu Phe Glu Leu Glu Asn Phe Val Ala Arg Gln Val Asp Val Ala Pro
 145 150 155 160

Ala Ala Ser Gly Ala Pro His Ala Ala Gly Gly Arg Leu

168 179

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Arg	Ala	Asp	Glu	Arg	Lys	Asn	Thr	Thr	Met	Lys	Met	Val	Lys	Ser	Ile
1															15

Ala	Ala	Gly	Leu	Thr	Ala	Ala	Ala	Ile	Gly	Ala	Ala	Ala	Ala	Gly	
				20					25					30	

Val	Thr	Ser	Ile	Met	Ala	Gly	Gly	Pro	Val	Val	Tyr	Gln	Met	Gln	Pro
				35				40					45		

Val	Val	Phe	Gly	Ala	Pro	Leu	Pro	Leu	Asp	Pro	Xaa	Ser	Ala	Pro	Xaa
				50				55					60		

Val	Pro	Thr	Ala	Ala	Gln	Trp	Thr	Xaa	Leu	Leu	Asn	Xaa	Leu	Xaa	Asp
				65				70			75		80		

Pro	Asn	Val	Ser	Phe	Xaa	Asn	Lys	Gly	Ser	Leu	Val	Glu	Gly	Gly	Ile
				85				90					95		

Gly	Gly	Xaa	Glu	Gly	Xaa	Xaa	Arg	Arg	Xaa	Gln					
				100				105							

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Val	Leu	Ser	Val	Pro	Val	Gly	Asp	Gly	She	Trp	Xaa	Arg	Val	Val	Asn
1										10					15

Pro	Leu	Gly	Gln	Pro	Ile	Asp	Gly	Arg	Gly	Asp	Val	Asp	Ser	Asp	Thr
				20				25					30		

Arg	Arg	Ala	Leu	Glu	Leu	Gln	Ala	Pro	Ser	Val	Val	Xaa	Arg	Gln	Gly
				35				40					45		

Val	Lys	Glu	Pro	Leu	Xaa	Thr	Gly	Ile	Lys	Ala	Ile	Asp	Ala	Met	Thr
				50				55					60		

Pro	Ile	Gly	Arg	Gly	Gln	Arg	Gln	Leu	Ile	Ile	Gly	Asp	Arg	Lys	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

65	70	75	80
Gly Lys Asn Arg Arg Leu Cys Arg Thr Pro Ser Ser Asn Glu Glu			
65	70	75	80
Glu Leu Gly Val Arg Trp Ile Pro Arg Ser Arg Cys Ala Cys Val Tyr			
130	135	140	145
Val Gly His Arg Ala Arg Arg Gly Thr Tyr His Arg Arg			
115	120	125	130

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Cys Asp Ala Val Met Gly Phe Leu Gly Gly Ala Gly Pro Leu Ala Val			
1	5	10	15
Val Asp Gln Gln Leu Val Thr Arg Val Pro Gln Gly Trp Ser Phe Ala			
20	25	30	35
Gln Ala Ala Ala Val Pro Val Val Phe Leu Thr Ala Trp Tyr Gly Leu			
35	40	45	
Ala Asp Leu Ala Glu Ile Lys Ala Gly Glu Ser Val Leu Ile Gln Ala			
50	55	60	
Gly Thr Gly Gly Val Gly Met Ala Ala Val Gln Leu Ala Arg Gln Trp			
65	70	75	80
Gly Val Gln Val Phe Val Thr Ala Ser Arg Gly Lys Trp Asp Thr Leu			
85	90	95	
Arg Ala Xaa Xaa Phe Asp Asp Xaa Pro Tyr Arg Xaa Phe Pro His Xaa			
100	105	110	
Arg Ser Ser Xaa Gly			
115			

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

(2) INFORMATION FOR USE IN NOSES.

4.3 SEQUENCES AND THEIR TYPES

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Val	Gln	Cys	Arg	Val	Trp	Leu	Glu	Ile	Gln	Trp	Arg	Gly	Met	Leu	Gly
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Ala	Asp	Gln	Ala	Arg	Ala	Gly	Gly	Pro	Ala	Arg	Ile	Trp	Arg	Glu	His
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32
Ser	Met	Ala	Ala	Met	Lys	Pro	Arg	Thr	Gly	Asp	Gly	Pro	Leu	Glu	Ala
33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48
Thr	Lys	Glu	Gly	Arg	Gly	Ile	Val	Met	Arg	Val	Pro	Leu	Glu	Gly	Gly
49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64
Gly	Arg	Leu	Val	Val	Glu	Leu	Thr	Pro	Asp	Glu	Ala	Ala	Ala	Leu	Gly
65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
Asp	Glu	Leu	Lys	Gly	Val	Thr	Ser								
81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96

(2) INFORMATION FOR SOC ID NO.:

(ii) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Thr Asp Ala Ala Thr Leu Ala Glu Glu Ala Gly Asn Phe Glu Arg Ile
 1 5 10 15

 Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly
 20 25 30

 Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala
 35 40 45

 Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Ile
 50 55 60

 Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
 65 70 75 80

 Ala Asp Glu Glu Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
 85 90 95

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met Thr Gln Ser Gln Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn
 1 5 10 15

 Arg Ala Asn Gln Val Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val
 20 25 30

 Pro Ile Thr Pro Cys Glu Leu Thr Xaa Xaa Lys Asn Ala Ala Gln Gln
 35 40 45

 Xaa Val Leu Ser Ala Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala
 50 55 60

 Lys Glu Arg Gln Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Xaa
 65 70 75 80

 Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly
 85 90 95

 Glu Gly Thr Val Gln Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser
 100 105 110

 Ser Ala Glu Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro
 115 120 125

Asn Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp
 130 138 140
 Gln Gly Ala Ser Leu Ala His Xaa Gly Asp Gly Trp Asn Thr Xaa Thr
 148 150 155 160
 Leu Thr Leu Gln Gly Asp
 158

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Arg Ala Glu Arg Met
 1 8

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Val Ala Tyr Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala Ala
 1 8 16 23
 Glu Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
 26 33 38 45
 Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
 38 43 48
 Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
 56 63 68
 Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe
 65 70 75 80
 Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
 85 90 95
 Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala
 100 105 110
 Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met

118	130	125
Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Glu Gly		
130	135	140
Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro		
145	150	155
His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met		
165	170	175
Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met		
180	185	190
Leu Lys Gly Phe Ala Pro Ala Ala Ala Gln Ala Val Gln Thr Ala		
195	200	205
Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly		
210	215	220
Ser Ser Gly Leu Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala		
225	230	235
Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Asn Ser Gly		
245	250	255
Arg Arg Asn Gly Gly Pro Ala		
260		

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Met Thr Tyr Ser Pro Gly Asn Pro Gly Tyr Pro Gln Ala Gln Pro Ala		
1	5	10
Gly Ser Tyr Gly Gly Val Thr Pro Ser Phe Ala His Ala Asp Glu Gly		
20	25	30
Ala Ser Lys Leu Pro Met Tyr Leu Asn Ile Ala Val Ala Val Leu Gly		
35	40	45
Leu Ala Ala Tyr Phe Ala Ser Phe Gly Pro Met Phe Thr Leu Ser Thr		
50	55	60
Glu Leu Gly Gly Asp Gly Ala Val Ser Gly Asp Thr Gly Leu Pro		
65	70	75
Val Gly Val Ala Leu Leu Ala Ala Leu Leu Ala Gly Val Val Leu Val		

88	90	98	
Pro Lys Ala Lys Ser His Val Thr Val Val Ala Val Leu Gly Val Ile			
188	195	110	
Gly Val Phe Leu Met Val Ser Ala Thr Phe Asn Lys Pro Ser Ala Tyr			
118	120	138	
Ser Thr Gly Trp Ala Leu Trp Val Val Leu Ala Phe Ile Val Phe Gln			
130	135	140	
Ala Val Ala Ala Val Leu Ala Leu Leu Val Glu Thr Gly Ala Ile Thr			
148	188	158	160
Ala Pro Ala Pro Arg Pro Lys Phe Asp Pro Tyr Gly Gln Tyr Gly Arg			
168	170	178	
Tyr Gly Gln Tyr Gly Gln Tyr Gly Val Gln Pro Gly Gly Tyr Tyr Gly			
180	185	190	
Gln Gln Gly Ala Gln Gln Ala Ala Gly Leu Gln Ser Pro Gly Pro Gln			
198	200	208	
Gln Ser Pro Gln Pro Pro Gly Tyr Gly Ser Gln Tyr Gly Gly Tyr Ser			
218	215	220	
Ser Ser Pro Ser Gln Ser Gly Ser Gly Tyr Thr Ala Gln Pro Pro Ala			
228	230	235	240
Gln Pro Pro Ala Gln Ser Gly Ser Gln Gln Ser His Gln Gly Pro Ser			
248	250	255	
Thr Pro Pro Thr Gly Phe Pro Ser Phe Ser Pro Pro Pro Pro Val Ser			
268	265	270	
Ala Gly Thr Gly Ser Gln Ala Gly Ser Ala Pro Val Asn Tyr Ser Asn			
278	280	285	
Pro Ser Gly Gly Glu Gln Ser Ser Ser Pro Gly Gly Ala Pro Val			
298	298	300	

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGAAGATGG TGAAATCGAT CGGCCCCGGT CTGAGCCGCC CGGCTTCGAT CGGGGGCGGT	60
CGGGCGGCTTG TGACTTCGAT CGGGCTGGAC GGCCCGGCTGC TGTACCGAGT CGGGCGGCTG	120

GTCTTCCCGG	GGCCACTGCC	CTTGACCCCG	GGATCCGCCC	CTGACCTCCC	GACCCCGCCC	140
CAGTTGACCA	GGCTTGCAA	CAGCCTTCCC	CATTCGACAG	TGTGCTTTGC	GAACAAAGGC	140
AGTCTGCTCG	AGGCGCGAT	GGGGCGGACC	GAACCGCTCA	TGCGCGACCA	CAACGTTAAG	190
AACGCCCCCG	ACGCGGAAAC	TCTTGCGCTG	TGTTCAAGG	TGACGAACNT	CCACGCCCCG	190
GGCGCGCTT	GGGGCGACCC	GGACGTTTCC	GTCTCGGCGC	CGAGCTCTC	GTGCGCGCTC	240
ACGGCGAACG	TCAGCTTCT	GAATCAGGC	GGCTGGATGC	TGTCACCGGC	ATCGGGCG	240
GGTTGCTTC	AGGGCGCAGG	GAATCTA				290

(2) INFORMATION FOR SEQ ID NO:95:

(A) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANGENESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala Ala Ala Ala						
1	5	10	15			
Ile Gly Ala Ala Ala Ala Gly Val Thr Ser Ile Met Ala Gly Gly Pro						
20	25	30				
Val Val Tyr Cln Met Qln Pro Val Val Phe Gly Ala Pro Leu Pro Leu						
35	40	45				
Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Cln Leu Thr Ser						
50	55	60				
Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala Asn Lys Gly						
65	70	75	80			
Ser Leu Val Glu Gly Gly Ile Gly Gly Thr Glu Ala Arg Ile Ala Asp						
85	90	95				
His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro Leu Ser Phe						
100	105	110				
Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala Thr Ala Asp						
115	120	125				
Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr Gln Asn Val						
130	135	140				
Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala Ser Ala Met						
145	150	155	160			

Glu Leu Leu Glu Ala Ala Gly Asn
165

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CATGGCCATT TCGTTGAGCC TCGGGGGCGG CTCGGGCTTC CGAGATCCCCG TGGACGCCGT	60
CATTAACACC ACCTTGAAATT AGGGGGAGGT ACTTGGCTTG CTCAACGCCA CGGGATGGGG	120
GGCTTCCGCAT GCTTCAACG CCTTGACCGT GCGCCATTTC TATTTGGCA ATTTCCTTAC	180
GGCGACCCCA CTCGAACGGG CTTCGATGSC CGCGGAAATTG CAACTTTCG CGGGGGCGAC	240
ACAGTACATC GCGCTTTCG AATGGTTTCG CGGCTCTTCG AACAACTATT AAGCCGACGG	300
GGGCCCCATC CGGGGGACGG CGATCTTCG CGGGCTTGG CGAGATTGCC CGGGCTCTCA	360
ACGGGGGCGA TCGGGGAGG CGGGGGATTC CGGGGGGCTA CGGGGGATTG CGGGGGCTCT	420
CGACGGGGCC CATCTCGATC CGGGGGGGG CGGGGGGGG CGGGGGCTCT TTCTAGAGCG	480
CGGGGGGGGG CGGGGGGGCT	500

(3) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Val Ala Met Ser Leu Thr Val Val Gly Ala Gly Val Ala Ser Ala Asp Pro			
1	5	10	15
Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Glu Val Val Ala			
20	25	30	
Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Glu Phe Asn Ala Ser			
35	40	45	
Pro Val Ala Glu Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro			
50	55	60	
Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala			
65	70	75	80

Gln Tyr Ile Gly Leu Val Gln Ser Val Ala Gly Ser Cys Asn Asn Tyr
as as as

(2) INFORMATION FOR SEC ID NO.: 988

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

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ATGACAGAGCC AGCGCTTGGAA TTTTGCGGT ATCGAGGCGTC CGCGAAGGC AATCGCGGGA 60
AATGTCAGCT CCGTTCAATT CGCTCTTGGAC GAGGGGGAGC AGTTTTCGAC CAAAGTCGCA 120
GGGGCGGCGG CGGGTGGCGG TTGGGAAAGCG TACC 184

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(2) INFORMATION FOR SEQ ID NO: 99:

(ii) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANGENESS: single
- (D) TOPOLOGY: linear

(ext) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Thr Glu Glu Glu Trp Asn Ser Ala Gly Ile Glu Ala Ala Ala Ser
1 5 10 15

Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
20 30 30

Lys Glu Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser
 38 39 40 41 42 43 44 45

Glu Ala Tyr
so

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1308;

CCGTGCGCGA CCTTCTGGTC ACTATGAAAG TCGCGTTGCG ATTCACGAT TCGTGAACCT 60
TCAAGCGCGCG AGGATCTACTG AGGTGCATCA TTAGCGACT TTTCGCGAAC ATGCTTGACG 120

CCTCCAAAACG CGGCCACAGCC GACGGTGTCTT CGCGCGAGGC GCTGTTTCGA AAATCCCTAA	180
GACAAATTGCG CGGGGGCGCC TACAAGGAAAG TCGCTCTGTA ATTCGCGCG TATCTGCTCG	240
ACCTGTTCG TCTTGACCGG GACGAAACCG TGCTTGACGT CG	282

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GATCTTACCC GTGCGTAACTGC TCGGGGCGTT TCGGATGCGA GTGCGACGTTG CTTCCTGAT	60
CGCGTACCGA GAGATGTTGC CGGGCGCGCC TGAACCGCTG CAGAGCATCG GTGCTTACCG	120
TCTCGCTTACG ATTCGCGCTG CGGGGGCGCC GAGGACTCGG GTGGTCCCCC CGCTCGCGA	180
TCAGGTTGCG GCGCTCACTG CGCGCGACTT CGCGCGCATG CGCGCGATGT ATCGATCGAT	240
GAGCGCTTG CGCTGGCGA TTTCATGACCA GTTCGCGCC ACCGTTGCGA CGAGCGCGAG	300
CTGCTATGCG CGCGCTGAGA TCGCCGAATGC CGGGCGCGCC AGCTTACCGA CGAACGCTCG	360
CGACCGAGAA CGCGCGAGAA TAGGGACCGG TAATGCTGAA TTTCGCGCGCC TTACGCGCG	420
AGATCAACTG CGCGAGGAGT TACGGCGCGCC CGGGTGGCG CGCGCGCGTG CGCGCGCGTC	480
AGATGCTGGA CGCGCGCGCG AGTGACCGTG TTTCGCGCGCC CGCGCGCGTT CGCGCGCG	540
TCTCGCTTACG CGCGCGCGCG TCGCTGATG CGGGCGCGCC CGCGCGCGTG CGCGCGCG	600
CGGGCGCGCA TCGGGCGCGCG ATCGACCGTG CGCGCGCGCA CGGGCGCGCG ACCGGCGCG	660
AGCGCGCGCG CGCTTACCGA CGCGCGATG CGGGTGGCG CGCGCGCGCG CGCGCGCGCG	720
CGATGCGCGA CGACCGCTTG CGACTGATGA TTTCGCGCGCC GACGACCGTC TTGGGGGAAA	780
ACACCGCGCG CGACCGCTTG AAccGACCGG AATACCGCGA CGATGCGCGA CGAGACCGG	840
CGCGCGATGT CGCTTACCGG CGCGCGACCG CGACCGCGAC CGCGCGATGT CGCGCGCG	900
AGCGCGCGCG CGCGCGCGCG CGCGCGACCG CGATGCGCGA TTGGGGCGCG CGCGCGCGAC	960
AGCGCGCGCG CGCGCGCGCG CGCGCGACCG CGATGCGCGA TTGGGGCGCG CGCGCGCGAC	1020
AGCTTACCGCG CGCGCGCGCG CGACCGACCG CGATGCGCGA TTGGGGCGCG CGCGCGCGAC	1080
CGGTCTCGCG CGATGCGCGCG CGACCGACCG CGATGCGCGA TTGGGGCGCG CGCGCGCGAC	1140

GTCGGCCACC GAGGCGAGG AGGGCTTCCC CGTGGCTCCC ATCGATTCG CTGGCTACTG	2886
GGTTTTCAG CCTTCCAGG CGCTTCCCGG CAGGTGGCC CGATTGCGG CGACGAGGC	2940
GGCTTGCCG TGGCTGGTGA CCACGCCAAC CGCCACAGG CGCGGGTGA CGAGTCGCG	3000
GAAGGAAACCC ACCCAGCCCG CGCGCTCTC CGCCGGCTG ACCTGGATTC CGAGGATC	3062

(2) INFORMATION FOR SEQ ID NO:102:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Met Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 1 5 10 15

Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp
 20 25 30

Asp Ser Val Ala Ser Asp Leu Phe Ser Ser Ala Ala Ser Ala Phe Gln Ser
 35 40 45

Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
 50 55 60

Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65 70 75 80

Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
 85 90 95

Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
 100 105 110

Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
 115 120 125

Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Gln Tyr Gly Glu Met
 130 135 140

Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala
 145 150 155 160

Thr Ala Thr Ala Thr Leu Leu Pro Phe Glu Gln Ala Pro Glu Met Thr
 165 170 175

Ser Ala Gly Gly Leu Leu Gln Gln Ala Ala Ala Val Glu Gln Ala Ser
 180 185 190

Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
 195 200 205
 Glu Gln Leu Ala Glu Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu
 210 215 220
 Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn
 225 230 235 240
 Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val
 245 250 255
 Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala
 260 265 270
 Ala Ala Ala Glu Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala
 275 280 285
 Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly
 290 295 300
 Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
 305 310 315 320
 Pro Gln Ala Trp Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
 325 330 335
 Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly
 340 345 350
 Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
 355 360 365
 Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met
 370 375 380
 Pro His Ser Pro Ala Ala Gly
 385 390

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GACGTCAGCA CCCGCCCGCC AGGGCTTGAG CGTGTGCGGT TTTGATGTGC GGTGAAAGTC	60
ACGTCGGCTGC CGCTGTGCGCC GCGCTTGAGC CAGACTGCGT AGCGCGCTTT AGTGGAAACTA	120
ATTTGGTTGA AGTGCGCTGC AGCTATAGGA CTTCACGATT GGTAAATGTA CGTTGACGCC	180

CCTGTTGGGC TCGATTTGTC CGAACAGTC CTGACCRAGC CTTGGCCCTTC CGGCCAGGC	240
CGCCATGAGA TGGCTTGACT ACCMATAAT CTGACCTTC CGGGCGGAGT CTGGCGCTAA	300
ATGACCGAGGA CGAACGCTGT CTTTCACCTC CGAACCGAG ATGTTGCGCG CGGGCGCTTC	360
CGAACCTTGT TGTTCGCG CGACCGTAA CGCTGAGA CGGGCGCG CGGGCGAC	420
GACTGGCTG CTGCGCGCG CGTGGACGA GGTGCGCTG CTGCTTCCCA CGAACGTTG	480
TACGGATGCG CGGACGATTC AGACGGCCAG CGCCGAGCG GCCTGATCC ATGACGTT	540
TETGACCG CGCGCCACCA CGGCTGTTG ATATGGCGAC ACCGGAGGCG CGAACGCTTC	600
CGTCACCGCC TAGCTGACTG CGGGTATTG CGGGCGAGG ATTATCGAAG TGTGGATT	660
CGGGCGCTTA CGACCGGAGA TGACTTCCC GAGGTGAC CGGGCGCG CGGGCGCTTC	720
CGGGCGCCCG CGGGCGAGA TUTGGAGAG CGGGCGACT GACCTTTTT CGGGCGCTTC	780
CGGGTTGAG CGGGTGTGCG CGGGCGCG CGGGCGAGT TGGATAGTT CGGGCGCTTC	840
TCTGATGCG CGGGCGCTT CGGGCGATG CGGGCGATG AGGTGACCG CGGGCGACCG	900
CGGGCGACCG CGGGCGCG CGGGCGCTG CGGGCGCG CGGGCGACCG CGGGCGACCG	960
GACGGTGGCG CGGGCGCTG CGGGCGCG CGGGCGACCG CGGGCGACCG CGGGCGACCG	1020
CGGGCGCTTC CGGGCGAGA CGGGCGAGA CGGGCGACCG CGGGCGACCG CGGGCGACCG	1080
CGGGCGCCCG CGGGCGAGG CGGGCGCTG CGGGCGCG CGGGCGACCG CGGGCGACCG	1140
CGGGCGCTTC CGGGCGAGG CGGGCGCTG CGGGCGCG CGGGCGACCG CGGGCGACCG	1200
CGGGCGACCG CGGGCGCTG CGGGCGCG CGGGCGACCG CGGGCGACCG CGGGCGACCG	1260
CGGGCGACCG CGGGCGAGG CGGGCGCTG CGGGCGCG CGGGCGACCG CGGGCGACCG	1320
CGGGCGCTG CGGGCGAGG CGGGCGCTG CGGGCGCG CGGGCGACCG CGGGCGACCG	1380
AGGGAAACAC CGACGTTGCA TGATGCGAC CGGGCGCTG ATGACCGAGA CGGGCGCTTC	1440
CGGGCGACCG CGGGCGCTG CGGGCGCG CGGGCGACCG CGGGCGACCG CGGGCGACCG	1500
CGGGCGCTG ATGACCGAGA CGGGCGCTG CGGGCGACCG CGGGCGACCG CGGGCGACCG	1560
CGGGCGCTG CGGGCGACCG CGGGCGCTG CGGGCGACCG CGGGCGACCG CGGGCGACCG	1620
CGGGCGACCG CGGGCGACCG CGGGCGCTG CGGGCGACCG CGGGCGACCG CGGGCGACCG	1680
CGGGCGACCG CGGGCGACCG CGGGCGCTG CGGGCGACCG CGGGCGACCG CGGGCGACCG	1740

(2) INFORMATION FOR SEQ ID NO:104:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 1 5 10 15

Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
 20 25 30

Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
 35 40 45

Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
 50 55 60

Leu Met Ala Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65 70 75 80

Ala Gly Gln Ala Gln Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
 85 90 95

Ala Tyr Glu Thr Ala Tyr Arg Leu Thr Val Pro Pro Pro Val Ile Ala
 100 105 110

Glu Asn Arg Thr Glu Leu Met Thr Leu Thr Ala Thr Asn Leu Leu Gly
 115 120 125

Gln Asn Thr Pro Ala Ile Glu Ala Asn Gln Ala Ala Tyr Ser Gln Met
 130 135 140

Trp Gly Glu Asp Ala Glu Ala Met Tyr Gly Tyr Ala Ala Thr Ala Ala
 145 150 155 160

Thr Ala Thr Glu Ala Leu Leu Pro Phe Glu Asp Ala Pro Leu Ile Thr
 165 170 175

Asn Pro Gly Gly Leu Leu Glu Glu Ala Val Ala Val Glu Gln Ala Ile
 180 185 190

Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
 195 200 205

Gln Gln Leu Ala Gln Pro Ala Gln Gly Val Val Pro Ser Ser Lys Leu
 210 215 220

Gly Gly Leu Trp Thr Ala Val Ser Pro His Leu Ser Pro Leu Ser Asn
 225 230 235 240

Val Ser Ser Ile Ala Asn Asn His Met Ser Met Met Gly Thr Gly Val
 245 250 255

Ser Met Thr Asn Thr Leu His Ser Met Leu Lys Gly Leu Ala Pro Ala
 260 265 270
 Ala Ala Gln Ala Val Glu Thr Ala Ala Glu Asn Gly Val Trp Ala Met
 275 280 285
 Ser Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu
 290 295 300
 Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser
 305 310 315 320
 Leu Ser Val Pro Pro Ala Trp Ala Ala Asn Gln Ala Val Thr Pro
 325 330 335
 Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Dln Thr
 340 345 350
 Ala Pro Gly His Met Leu Gly
 355

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3027 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

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AGTTTCAGTCG AQAATGATAAC TGACCGGCTG TATCCACGT CCTCTGAAGCA ATGGAAAC 60
CGTCCGACGC CGGGACATCG CAASCCACCG CGATGGGTT CGGGGGGAA CGTAAACCD 120
CCGAAGCCGA AGGGCTGCCG CGCCGGGGCG CGGGCTGGCG CGCTGGGGCG CGTGGAGGC 180
CTGAGGGCGT CGGGATGGCG CGAGCGGGG ACCAGAACGT CGCCGAGGAT ATGGAGACTG 240
CGAAGACGCCG GAAGACTATGA ACCCTATAGC CGCGCAGACG ACCAGACCG 300
ACGTTGGCA TCTTGCGAC GGCGTTGG CGTCCGGTTA CCAAGACTGT CGACGATTG 360
CATGGGTTG CGACTCTCA TCATCTGGG CTTCACCGG CGTACGGGAT ACATTGTGTC 420
CGAACACCAT GAGGGGACCG AACGGCGGCA CGGGGGCG CGGTTGGGG CGGGAGCCAA 480
CGAAGGTGTC ATGAAACATGA CGTGGCTGGA CTTCACGAG CGCGAAAGAAG ACCTTGCGCG 540
TGTGATCGAC AGCTCCGACCG CGGAATTGAG CGATGACTTC CACCGGGCG CGGGCGTTT 600
CACCAAGTT GTCGAACAGT CGAAAGCTGT CGGGAGACG ACCGTAACG CGACGCGTT 660
CGATCCATG AACGACGATT CGGGCGTGTG CGTCTTCGG CGGACTTGC CGGTGACCA 720

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TTCGGCTTGC	CCGAAAGCG	AACCAACTGC	GTCGGCGCTC	AAAGCTACCG	TGACCGAAGA	780
CGGGGACAG	TACGAGATGT	CGAAACTTGA	TTTCCTTACCG	TGACCGATGA	CGTACGCCAC	840
CTCAACACCG	AAACCAACTGA	CCCCACCAA	TTGGCTTAAA	TGACTCACC	CGCAAGCGAA	900
GGCGTTGATT	CGGGGACCGA	GGCATTTGAC	ACCGACTCTG	CAACCGAATC	TACCGCCGAG	960
AACGGCTTAC	CCCCACCTGA	CGCTTGCGA	ATTCAGGTTA	CCTTGAAACC	CGTTCCGCTG	1020
ATTCCTCATCC	TGCTCTGTT	GAATCTTGG	GGGGGACCG	GTGGGTATA	CCTTGAGGAA	1080
TACCGACCGA	TGGCGAGCC	GACTCGGG	CCCCACCTGC	TTCCGCTAAC	GGGGCGCTG	1140
ACCGACGAT	CCCCCTTTC	TGATTTGCG	GGACACCGTG	ACCAAGACCT	CGCTTACCCG	1200
ACGTCGACCC	TGACCGCCGA	TTTCCTTTC	TATACGACCA	TTTCACCGCG	CGATCGTGC	1260
CTGGGGCG	CAACACGAAG	TGACTGAAA	CCACCGCGA	CGCTCTGCG	GGGGCGGTGT	1320
CGGAGCTACA	TCCGATTGCG	CCGCTGTTTC	TGGTTTTGCT	CGACCGAGCC	ACTACCGATA	1380
ACCGACGCTC	CAATCCGTCG	ATGGGGCGCA	CGAGCGTGAT	GGTGACCGTA	GGCAAGCTCG	1440
ACGGCAATTC	CTTGATCACG	AACTTGCCTC	CGTTTTAGGT	TGCGTACGCC	CGTGCCCAAG	1500
TGTCACCGCC	GGGGGGGTGC	CTTGCTTCTC	GGATACCCCG	CGTTCTTCCG	GGATATCAG	1560
CCCCACCTTC	AAACGAGATGT	CCCCACCTGT	CTAATCGGCC	GGTTTATTA	AGATTAGTTC	1620
CGACCTTATT	TACCTGATGT	TCAGATTGTT	CGCTCGATT	TGCTTGGC	GGGGGGCGC	1680
TGTTTAACTT	TCATCTGG	CTTGTGACTA	TTTGAGAGA	TTTGACCTGT	TGCGACGTT	1740
TTTTGCTTTC	CGATCTTGT	CTTGTGATG	GGGACCGA	ACGATTATCG	AACTGCTGCA	1800
CTGGGGCG	TTACCCACCG	AGATCAACTC	CGCGAGGATG	TGCGTACGCC	CGGGTTGGU	1860
CTGGGGCG	CCCCCGCGA	AGATGTGGCA	CGCGTACCGG	AGTGACCTGT	TTTCGGCGCC	1920
CTGGGGCGTT	CACTCGCTG	TGCGTACCGT	GGCGACCGGA	TGCGTACCGG	GTGGCTCGCC	1980
CGGTGTGATG	CTGGGGCGCG	CTTGGCGCTA	TGCGTACCGG	ATGACCTGT	GGGGGGCGCA	2040
GGGGGGCGTG	ACGCGACGCC	AGGTGCGGT	TGCTTGGCG	GGCTTACCGA	CGGGTACCGG	2100
CTGGGGCGTG	GGGGGGCGCG	GGATCCGCGA	GAACCTGT	GAATGATGGA	TTCTGATAGC	2160
GACCGACCTC	TTGGGGCGAA	ACACCGCGGC	GTGGCGGT	AACTGGGCC	AAATACGGGA	2220
GATGCGGCGT	CAAGACGCCG	GGCGATGTT	TGCGTACCGG	GGCAACGGCG	CGACGGCGAC	2280
CGGGGGCGTG	CTGGGGTTCG	AGGACCGGGC	ACTGATCACG	AACTGGGCC	GGCTTCCCTGA	2340
GGGGGGCGTG	GGGTGCGAGG	AGGACCTGCA	GGGGGGCGCG	GGGGACCGGT	TGATGAAACAA	2400

TCTGCCCCAA	GGCTTGAC	AACCTGCCCA	GGCCACAAAA	AGCATCTGCG	CCTTCGACCA	2460
ACTGAOTGAA	CTTGTGAAAC	CGATCTGCC	GCATCTGCG	CGCTCTGCA	ACATGCTGTC	2520
GATGCTGAC	AACCACGTGT	GGATGACCAA	CTGGGGTGTG	TGATGCGCA	GCACCTTGA	2580
CTCAATGTTG	AAGGGCTTTC	CTTGCGGGCC	GGCTCACGGCC	CTGGAAACCC	CGCGCGAAAA	2640
CGCGCTGAG	GGATGACT	CGCTGGCG	CGCTGGGT	TGCTGCGT	CTGCTGGC	2700
TCTGGCGCT	GGCTGCGG	CGAAGTGG	TCGGGGGCC	TGTTGCGTT	CGTGTGGT	2760
GGCGCGGCC	TGGCGCGG	CGAACGGAC	CGTGTGGCG	GGCGCGGCG	CGCTGGCGT	2820
GACCGACCGT	ACCGCGGCC	CGAAACCGC	CGCGGACAC	ATGCTGGCG	CGCTGGCGT	2880
GGCGCAACTG	ACCAATGCG	CGCGCGGTT	CGCGGGGTT	ACCAATGCG	TGCGATGCC	2940
GGCGCGGCC	TACCTGATTC	CGCTGTGCG	CGCGCGGCC	TAACCGCGAT	CGCGACGCGA	3000
TGCGCGCGT	CTATGGCGAC	AGCGATC				3027

(2) INFORMATION FOR SEC ID NO:1061

(3) SEQUENCE CHARACTERISTICS.

- (A) LENGTH: 396 amino acids
- (B) TYPE: amino acid
- (C) STRANGENESS:
- (D) TOPOLOGY: linear

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
35 36 37 38 39 40 41 42 43 44 45 46 47 48

Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
38 39 40 41 42 43 44 45 46 47 48 49 50

Asp Ser Val Ala Ser Asp Leu Phe Ser Ser Ala Ala Ser Ala Phe Glu Ser
35 36 37 38 39 40 41 42 43 44 45

Val Val Trp Gly Leu Thr Thr Gly Ser Trp Ile Gly Ser Ser Ala Gly
SC SC

Lau Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
aa aa

Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
aa aa

Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
100 200 300 400

Glo Aan Arg Ais Glo Lou Mer Tle Lou Ille Als Tey Aen Lou Lou Giv

115	120	125
Ser Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met		
130	135	140
Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Thr Ala Ala		
145	150	155
Thr Ala Thr Glu Ala Leu Leu Pro Phe Glu Asp Ala Pro Leu Ile Thr		
165	170	175
Asn Pro Gly Gly Leu Leu Glu Gln Ala Val Ala Val Glu Glu Ala Ile		
180	185	190
Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu		
195	200	205
Gln Gln Leu Ala Gln Pro Thr Lys Ser Ile Trp Pro Phe Asp Gln Leu		
210	215	220
Ser Glu Leu Trp Lys Ala Ile Ser Pro His Leu Ser Pro Leu Ser Asn		
225	230	235
Ile Val Ser Met Leu Asn Asn His Val Ser Met Thr Asn Ser Gly Val		
240	245	250
Ser Met Ala Ser Thr Leu His Ser Met Leu Lys Gly Phe Ala Pro Ala		
260	265	270
Ala Ala Gln Ala Val Glu Thr Ala Ala Gln Asn Gly Val Gln Ala Met		
275	280	285
Ser Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu		
290	295	300
Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser		
305	310	315
Leu Ser Val Pro Gln Ala Trp Ala Ala Asn Gln Ala Val Thr Pro		
320	325	330
Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr		
340	345	350
Ala Pro Gly His Met Leu Gly Gly Leu Pro Leu Gly Gln Leu Thr Asn		
355	360	365
Ser Gly Gly Gly Phe Gly Gly Val Ser Asn Ala Leu Arg Met Pro Pro		
370	375	380
Arg Ala Tyr Val Met Pro Arg Val Pro Ala Ala Gly		
385	390	395

(I) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(II) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CATCGGAGCC	ACTGATCACCC	ATGCTGTGCC	ACCCGATGCC	ACCGGGACTAA	ATACCCGAC	60
GCTGATGCC	GGCGCGGTC	CGGCTTCAAT	CTTTCGCCG	GGCGCGGAT	GGCGAGCTT	120
TTCGGCGCT	CTGGGACGTC	ACGGCGCTGA	CTTGACCGCG	CGCCCTGAACT	CTCTGGGAGA	180
ACCCCTGACT	GGAGGTCGA	GGGACGAGGC	CTTTCGCGCT	GGAGCTCCGA	TTGGTTCGTC	240
GCTTACAAACC	GGTTCGACAC	AGGCGTACAC	CTTTCGCGAT	CGGGCGACG	GGCAAGCTC	300
GGCATACACT	GGGGCGATAC	CTGGGACGGC	CTGGGCGCT	GGATGGCCCG	CGAACCGAT	360
CGACCGACCC	CTGCTTACGG	CCACCAAATT	CTTTCGCTATC	AACACGATCC	CGATCGCTT	420
GGCCGAGATG	GATTATTCGA	TCGCTATGTG	GAACCAAGCA	GGCCTGGGAA	TCGAGGTGA	480
CGAGGCCGAG	ACCGGGTTTA	ACAGGCTTTT	CGAGGAGTC	GGCCGATTCG	CTTTCGATCT	540
TGATCCCGCC	GGGACCCGAA	GGCGATTCG	GGAAATGCCG	GGCCGCGAC	CTGACACCG	600
CTGACACCC	CTTTCGCGAT	TCGCGCCCG	GGTACCGAG	ACCTCGCCG	AACTCGTTGA	660
GATTACGCC	GGGATCGAGC	AGTTCGACCA	GGCTTTCAG	CGGGTCACT	CTTTCGTCAG	720
CGACCGACCC	GGGACCCGAA	GGCGATTCG	GGGGCGCG	GGGGCGCG	ACGTCGCGCT	780
CTTTCGCGCC	AGTCGCGCT	GGAAACCTTC	GGTACCGAG	ACCTCGCCG	GGGGCGCG	840
GGCGCGATG	CTGGGCGCG	AGTTCGACCC	GGGGCGCG	GGGGCGCG	GGGGCGCG	900
GGGGCGCGCT	GGGGCGCGAT	AAAAGCCGCT	TCGCGCCCG	GGGGCGCG	GGGGCGCG	960
GGGGCGCGCT	GGGGCGCGAT	GGGGCGCGAT	GGGGCGCG	GGGGCGCG	GGGGCGCG	1020
GGGGCGCGAT	GGGGCGCGAT	GGGGCGCGAT	GGGGCGCG	GGGGCGCG	GGGGCGCG	1080
TGAAGAAGAC	GACGAGGACCC	ACTGGGACCA	AGAGGACGAC	TCGTCAGCTC	GGTTCGATAC	1140
AAACGAGCTTC	CGCGCCACCC	GGGGCGCGAG	ACTTTCGTCAC	ATTTTGGCGA	GGGACGTTAA	1200
GAGAGAAAGT	AGTCGCGAT	GGCAGAGATG	AGAGGACGAT	GGTTCGACCT	GGGGCGCG	1260
GGGGCGCGAT	GGGGCGCGAT	GGGGCGCGAT	GGGGCGCG	GGGGCGCG	GGGGCGCG	1320
GGGGCGCGAT	GGGGCGCGAT	GGGGCGCGAT	GGGGCGCG	GGGGCGCG	GGGGCGCG	1380
GGGGCGCGAT	GGGGCGCGAT	GGGGCGCGAT	GGGGCGCG	GGGGCGCG	GGGGCGCG	1440

ACGATTCGAGCTTGTATCGGGGAGGCGCCGAGGCGGCGAAGGGCGCG

TCCTCGGAA TGGGCTTGTG ACCCGCTTAAT ACCGAAAAGAA ACTGAACTAAA AACATGAGAG

AGCAGCCAGTC GAAATTTCGCG CCTATCGAGG CGCGCGGCAAG CGCAATCGG CGAAAT

(2) INFORMATION FOR SEQ ID NO:108:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xx) SEQUENCE DESCRIPTION: SEQ ID NO:106.

EDUCATIONAL ACTIVITIES

GCAGCGCGGGC GGAAGACGAG CACTGGGGTC GAAGAAACGGT TGGCGCTGCGG 18

AGCTTCCATA CCTTCGATCC GCGGGAAAGCG CTTCATGTTAA TCGGGCGGCGA TCGGAACTG

TCAGACTGCG CTGAAACGTA TAAACACGAG AAAACGGCGAG ACCGAGCGAA CGTCGAATC

GGCGGATCC GGTTCGCT ATTCTACGCG AACTCGGGGT TGCCTTATGC GAACTTCCA 303

GTGACGTTTGCTTCGGTGAACCGATTCG TGACCGCTTG GCGTCAAGCTT CGCGCCCGGC 380

TTTCGCGCGG CTTTGTTCAG CTCCGCTAGCC GTCGGCGTCAG ATTTCGTCGCA GACACGTTGGC 4336

1980-1981 1981-1982 1982-1983 1983-1984 1984-1985 1985-1986 1986-1987 1987-1988 1988-1989 1989-1990

(2) INFORMATION FOR SEQ ID NO:109:

SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 168 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

Met Leu Trp His Ala Met Pro Pro Glu Xaa Asn Thr Ala Arg Ieu Met

Ala Gly Ala Gly Pro Ala Pro Met Leu Ala Ala Ala Ala Gly Trp Gln

Thr Leu Ser Ala Ala Leu Asp Ala Glu Ala Val Glu Leu Thr Ala Arg

Ieu Asn Ser Ieu Gly Glu Ala Trp Thr Gly Gly Gly Ser Asp Lys Ala
58 59 60 61 62

Leu Ala Ala Ala Thr Pro Met Val Val Tryp Leu Gln Thr Ala Ser Thr
 85 79 75 80
 Gln Ala Lys Thr Arg Ala Met Gln Ala Thr Ala Gln Ala Ala Tyr
 85 90 95
 Thr Gln Ala Met Ala Thr Thr Pro Ser Leu Pro Glu Ile Ala Ala Asn
 100 105 110
 His Ile Thr Gln Ala Val Leu Thr Ala Thr Asn Phe Phe Gly Ile Asn
 115 120 125
 Thr Ile Pro Ile Ala Leu Thr Glu Met Asp Tyr Phe Ile Arg Met Tryp
 130 135 140
 Asn Gln Ala Ala Leu Ala Met Glu Val Tyr Gln Ala Gln Thr Ala Val
 145 150 155 160
 Asn Thr Leu Phe Glu Lys Leu Glu Pro Met Ala Ser Ile Leu Asp Pro
 165 170 175
 Gly Ala Ser Gln Ser Thr Thr Asn Pro Ile Phe Gly Met Pro Ser Pro
 180 185 190
 Gly Ser Ser Thr Pro Val Gly Gln Leu Pro Pro Ala Ala Thr Gln Thr
 195 200 205
 Leu Gly Gln Leu Gly Glu Met Ser Gly Pro Met Gln Gln Leu Thr Gln
 210 215 220
 Pro Leu Gln Gln Val Thr Ser Leu Phe Ser Gln Val Gly Gly Thr Gly
 225 230 235 240
 Gly Gly Asn Pro Ala Asp Gln Glu Ala Ala Gln Met Gly Leu Leu Gly
 245 250 255
 Thr Ser Pro Leu Ser Asn His Pro Leu Ala Gly Gly Ser Gly Pro Ser
 260 265 270
 Ala Gly Ala Gly Leu Leu Arg Ala Glu Ser Leu Pro Gly Ala Gly Gly
 275 280 285
 Ser Leu Thr Arg Thr Pro Leu Met Ser Gln Leu Ile Glu Lys Pro Val
 290 295 300
 Ala Pro Ser Val Met Pro Ala Ala Ala Gly Ser Ser Ala Thr Gly
 305 310 315 320
 Gly Ala Ala Pro Val Gly Ala Gly Ala Met Gly Gln Gly Ala Gln Ser
 325 330 335
 Gly Gly Ser Thr Arg Pro Gly Leu Val Ala Pro Ala Pro Leu Ala Gln
 340 345 350
 Gln Arg Gln Glu Asp Asp Gln Asp Asp Trp Asp Gln Gln Asp Asp Trp

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380

13

(2) INFORMATION FOR SSO ID NO:110:

4.1 SEQUENCE CHARACTERISTICS

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Ala Glu Met Lys Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly
1 6 10 15

Asn Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val
28 29 30

Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly
 35 43 45

Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys
50 55 60

Gln Lys Glu Glu Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly
65 70 75 80

Val Glu Tyr Ser Arg Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser
 85 86 87 88

Ser Met Gly Phe
100

INFORMATION FOR

(2) INFORMATION FOR SEQ ID NO:2111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1&:

```

GATCTTCCCGC GACCTTAAAA CCCAGATCCA CCAGCTGGAG TCGACCGGCG GTTCCTTTCA 60
CGGCACTTG CGGCGCGGG CGGGGAGGCC AGTCCTAGGCC CGGTCTGGGC GCTTCGAGA 120
AGCGACCAT AAGCGAAAGC AGGAACCTCGA CGAGATCTCG ACCGATATTG CTCAAGCCCG 180
CTTCCATTCG TCGACGGGCC ACCAGGAGCA CGACCGGGG CTGTCTCTGC AAATGGGCTT 240
CTGACCCGCT AATACGAAAAA CAAGACCGACC AAAAACATCA CAGACCCGCA GTGGAAATTG 300
ACCGATTTG AGCGCTGGCC AAGCGGATTC CGGGGAAAGC TCGACCTGGAT TGTTCGGTC 360

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CTTGACCAAG CGAACGACTC CCTGACCAAG CTCGCA

396

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Ile	Ser	Gly	Asp	Leu	Lys	Thr	Gln	Ile	Asp	Glu	Val	Ser	Thr	Ala
1														15

Gly	Ser	Leu	Gln	Gly	Gln	Trp	Arg	Gly	Ala	Ala	Gly	Thr	Ala	Ala	Gln
														30	

Ala	Ala	Val	Val	Arg	Phe	Gln	Glu	Ala	Ala	Asn	Lys	Gln	Lys	Gln	Glu
														35	

Leu	Asp	Glu	Ile	Ser	Thr	Asn	Ile	Arg	Gln	Ala	Gly	Val	Gln	Tyr	Ser
														50	

Arg	Ala	Asp	Glu	Glu	Gln	Gln	Ala	Leu	Ser	Ser	Gln	Met	Gly	Phe
														55

														60
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(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CTGGATCCCG	ATCCCCCTTTT	TCGCTTTTCT	ACGCCAACTC	GGCGTTACCC	TATGCCACA		60
TCCCACCTAC	CTTCGCTTTCG	GTCGAACCCA	TTGCGTTTAC	GGCTTCGTTG	ATCGTCGCG		120
CCGGTTTGT	CGGGGCTTTC	TTGAGCTTCC	TAGCCCTTCC	CTGGCGTTTT	TCTGGACAC		180
CCTGGTACCC	CTTCGAAACCG	CTACCCCTCCC	AGGGCGCTTC	GGCTTTCGTC	AGGGACTGCT		240
TCCCGCTTC	AAGGAGGGAA	TGATGGACG	TGACATTTCG	CTGGGTTCCG	CTTGCCCGGG		300
CTTCGATACC	GGCGGAAATTG	CACTGCTCTT	CTGTCATGTT	TTTGCTCGGT	TTCTTTTGCT		360
ATTAGGCGGT	CAGLAGGCCA	TTTSCCGA					387

(2) INFORMATION FOR SEQ ID NO:114:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CGCCACCAAGG ATTCGGTTG CCCCAACGCC CCTTCCGAGG GCTCCCTTCC GGGGGGAGC	60
TGGGGGGGGG ATGCTTCTTC TGCCTTACGC CGCTCTGGA TGGATGGACC AGTTCTTAC	120
TTCCCGACGT TTCCCTTGAT CTCTCTGCGA TAGCGCTGAC CCCGGCGGCC ACUTCGGGG	180
TUTTGCGGG CGGGCGGT CGCTGTTGC CGGGCGGTG CAGACGCTCT CGACCGAAAC	240
CGCGGGGCGT CGGGCGGTG CAGCTTGGCC CA	272

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Asp Pro Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Glu Val			
:	5	10	15
Val Ala Ala Leu			
20			

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Ala Val Glu Ser Gly Met Leu Ala Leu Gly Thr Pro Ala Pro Ser			
2	5	10	15

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala Ala Lys
1 5 10 15

Glu Gly Arg

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp Pro Ala Trp Gly Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:III:

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro
1 S 10 18

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(2) INFORMATION FOR SEQ ID NO:132:

(2) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Ala Pro Lys Thr Tyr Xaa Glu Glu Leu Lys Gly Thr Asp Thr Gly
11 12 13 14 15

(2) INFORMATION FOR SEQ ID NO:123:

(ii) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gin Ieu Thr Ser
 1 6 10 15

Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Thr Ala Asn
39 28 30

(2) INFORMATION FOR SEQ ID NO:124:

DNA SEQUENCES CHARACTERISTICS

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANGENESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

Asp	Pro	Pro	Asp	Pro	His	Gln	Xaa	Asp	Met	Thr	Lys	Gly	Tyr	Tyr	Pro
+				+					+					+	

Gly Gly Arg Arg Xaa Phe
29

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Asp Pro Gly Tyr Thr Pro Gly
1 5

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: /note= "The Second Residue Can Be Either a Pro or Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Xaa Xaa Gly Phe Thr Gly Pro Gln Phe Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: /note= "The Third Residue Can Be Either a Gln or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Xaa Pro Xaa Val Thr Ala Tyr Ala Gly
1 5

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Xaa Xaa Xaa Glu Lys Pro Phe Leu Arg
1 5

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Xaa Asp Ser Glu Lys Ser Ala Thr Ile Lys Val Thr Asp Ala Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Ala Gly Asp Thr Xaa Ile Tyr Ile Val Gly Asn Leu Thr Ala Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Ala Pro Glu Ser Gly Ala Gly Leu Gly Gly Thr Val Gln Ala Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Xaa Tyr Ile Ala Tyr Xaa Thr Thr Ala Gly Ile Val Pro Gly Lys Ile
1 5 10 15

Asn Val His Leu Val
20

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 682 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GCAGACGCTT CCTGGGTTTTT CGGTGGATCG GTTGGGGTCG GCTGGCGTCG	60
TCAACGATCG ACCGACCCCGA CCTTCGAAAC CGTTAGAGGG AGCGCGAACG CGCTGGCG	120
CGAACGTTCAT CGGTTTGGT CGGACGCGAAC AGCGACGCCG CGTACCGCCG CGTACCGCCG	180
ATGATCGAAC CGTGGGATTG CAGGGCGCGA CGATTCGGCG TGTACAGLAC GTGGTGCGCG	240
CGCGCGGTAC CTGACCGGGG CGTGGCTGGA CGCGCGCTTC CGTGGCGTCG GAAGCGCGCG	300
CGCTGGCGCG TTGTTCGCT CGCGCGCTTC CGATCGCGCT CGCGCGCGCTT ATTCGGCGCG	360
TCCCCGGTTC CGACGCTGGA ATGCCGACCA TCCCCACCGCG ACCGCGACG ACGCCGGTGA	420
CGCGCGCGCG CGACGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	480
CGACGCGCG CGACGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	540
CGACGCGCG CGACGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	600
CGCGCGCGCG CGACGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	660
CGACGCGCG CGACGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	720
CGACGCGCG CGACGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	780
CGACGCGCG CGACGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	840
CGACGCGCG CGACGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	882

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

CCATGAGA	ACCGCTTCCC	GGGCGGGGAC	CCCCGGGTAC	GGCTTGACCC	CCACGCCCGC	60
CGCTTCCTTC	GGTGGCGGGG	TTCGGGGGCT	GGGGGGGATC	GGGGGGGCTC	GGCTGGGGTC	120
CTAAGGGGTT	GGTACCGGGG	TGTTGGGGG	GGGGGGGCT	GGGGGGGCTC	GGCTGGGGTC	180
TGGGGGGGTT	GGGGGGGCT	GGGGGGGCT	GGGGGGGCT	GGGGGGGCTC	GGCTGGGGTC	240
GGGGGGGCTC	GGGGGGGCT	GGGGGGGCT	GGGGGGGCT	GGGGGGGCTC	GGCTGGGGTC	300
TGGGGGGGCT	GGGGGGGCT	GGGGGGGCT	GGGGGGGCT	GGGGGGGCTC	GGCTGGGGTC	360
ACGGGGGGTT	GGGGGGGCT	GGGGGGGCT	GGGGGGGCT	GGGGGGGCTC	GGCTGGGGTC	420
GGGGGGGCTC	GGGGGGGCT	GGGGGGGCT	GGGGGGGCT	GGGGGGGCTC	GGCTGGGGTC	480
CACTTGGAG	GGGGGGGCT	GGGGGGGCT	GGGGGGGCT	GGGGGGGCTC	GGCTGGGGTC	540
ACGGGGGGTC	GGGGGGGCT	GGGGGGGCT	GGGGGGGCT	GGGGGGGCTC	GGCTGGGGTC	600
GGGGGGGCTC	GGGGGGGCT	GGGGGGGCT	GGGGGGGCT	GGGGGGGCTC	GGCTGGGGTC	660
ACGGGGGGCT	GGGGGGGCT	GGGGGGGCT	GGGGGGGCT	GGGGGGGCTC	GGCTGGGGTC	720
ACGGGGGGCT	GGGGGGGCT	GGGGGGGCT	GGGGGGGCT	GGGGGGGCTC	GGCTGGGGTC	780
GGGGGGGCTC	GGGGGGGCT	GGGGGGGCT	GGGGGGGCT	GGGGGGGCTC	GGCTGGGGTC	840

(ii) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACGGGGGGCT	GGCTGAGGTC	TGAGATCAGA	GAGTGTCCCG	ACTCACCGG	GGGGGGGCTC	60
CTTCTCCCCG	AACAACCTCT	GAAGATCTTC	GGGGGGGAA	CAGGGGCTCA	TTTGACGGCTC	120
TATGGGGGTT	TGAACGACCA	GATCATCGG	CAGATTGATA	TGGGGGGGCT	GGGGGGGCTC	180
GGGGGGGCTC	TGTTGGGGCT	GAATGGGCTG	GGGGGGGCT	GGGGGGGCTC	GGCTGGGGTC	240
GGGGGGGCTC	TGTTGGGGCT	GAATGGGCTG	GGGGGGGCT	GGGGGGGCTC	GGCTGGGGTC	300
GGGGGGGCTC	TGTTGGGGCT	GAATGGGCTG	GGGGGGGCT	GGGGGGGCTC	GGCTGGGGTC	360
GGGGGGGCTC	TGTTGGGGCT	GAATGGGCTG	GGGGGGGCT	GGGGGGGCTC	GGCTGGGGTC	420

ACACCCGAGC TGTCTTACGCC ACCCGGGTC CGTCAGGAAAG TTGACCGAAC CGACGATCT	480
GGCTTCTGCC TGTCTTTAAG CGACGGATC GTGTCAGGAA AGATCTTAA TGAGCAGGCC	540
TTGATTGCG CGACGACGTC CGGGCGAGAC GTTGTCTTAA GAATCCGAC GATGAAGCAG	600
TGCTTGCCG CGGTGATCG ATGGGGTC CGGGCGAGT TAAACGGTT CGAGGGAAAT	660
CGCGAAAGG CATACTTCAC CGGGCGAGG CGATCTGATC CGAGGGTT CGATTTGCG	720
CGGGCTCAA CGGGCGAGG TTGGACGCC TTGACCTAA TGCTTGCCG CGGTGATCG	780
CGCTCTCAA AGGACGATC AGGGCGATC GGCGCTCAA CGCTGAGGCC GTATATGGGT	840
TTCTTACACC AGGGCGATC AGGGCGATC ACCTGATCG CGGAATTGCG CGGGCGAGC	900
ACTTAACCG CGGGCGAGT CGTCACTTAA CGTCACTTAA CGGGCGAGG CGGGCGAGC	960
CGGGCGCTTA ATGACGAGAG ATGGGGTC CGGGCGAGC CGGGCGAGT CGGGCGAGC	1020
ATACCGGGCG CGACGACGTC CGGGCGAGC AGGGCGATC CGGGCGAGC CGGGCGAGC	1080
CGGTGATCG CGGGCGAGC CGTCACTTAA TGACCTGCG CGGGCGAGC CGATGGCTGC	1140
TTGGCGGAG AG	1152

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

CGCTCTGCGA TTGGCGGAGG TGTACTTTGC CGCTCTTAAAG CGCGCATGAG TGCCGAGAAC	60
CGCGAACTCC CGACGACGAC CGATCCCGCT CGACGACGCC ACCCGGTCGA CGTGGCGCAT	120
CGCTCTGCGA CGCGCTTAAAG CGGTCTTTTC CTGGCGGAGG CGATCTGAGC GTTGTTCGCG	180
CGCTCTTTCG CGCGCTTAAAG CGCGCTTAAAG CGGTCTGGCG CGCGCTTAAAG CGCGCTTAAAG	240
ATGAGCACAC CGCGCTTAAAG CGTCTGAGA AGCTTGTGAG CGCTGAGGCC CGCGCTTAAAG	300
CGCGCTTAAAG CGTCTGAGA GAAGTGTGAG CGCGCTTAAAG CGTCTGAGA CGCGCTTAAAG	360
TGAGGCGAGC CGTCTGAGA CGCGCTTAAAG CGGATGGCG CGTCTGAGA CGTCTGAGA CGCGCTTAAAG	420
TTGGCGGAGC CGACGACGTC CGTCTGAGA CGGATGGCG CGTCTGAGA CGTCTGAGA CGCGCTTAAAG	480

TCCCGACACT GTCGGGTTT GCGCGGAA AGCGCGGT CGGTGCGGT CGGTGATTC	540
TCACCGCGC CGGACTAAC CGCGCTGCC CGCGCGATGT CGGTGCGGC CGGTGATTC	560
TCGGCGTTCAT ACTCTTCAAC CGCTCGGGG AACAGCTGA TTCCCGGAGCC CGCCA	580

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Asn Ala Val Val Ala Phe Ala Val Ile Gly Phe Ala Ser Leu Ala Val			
1	5	10	15

Ala Val Ala Val Thr Ile Arg Pro Thr Ala Ala Ser Lys Pro Val Glu		
20	25	30

Gly His Gln Asn Ala Gln Pro Gly Lys Phe Met Pro Leu Leu Pro Thr		
35	40	45

Gln Gln Gln Ala Pro Val Pro Pro Pro Pro Asp Asp Pro Thr Ala		
50	55	60

Gly Phe Gln Gly Gly Thr Ile Pro Ala Val Gln Asn Val Val Pro Arg			
65	70	75	80

Pro Gly Thr Ser Pro Gly Val Gly Gly Thr Pro Ala Ser Pro Ala Pro		
85	90	95

Glu Ala Pro Ala Val Pro Gly Val Val Pro Ala Pro Val Pro Ile Pro		
100	105	110

Val Pro Ile Ile Ile Pro Pro Phe Pro Gly Trp Gln Pro Gly Met Pro		
115	120	125

Thr Ile Pro Thr Ala Pro Pro Thr Thr Pro Val Thr Thr Ser Ala Thr		
130	135	140

Thr Pro Pro Thr Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr			
145	150	155	160

Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr Thr Pro Pro Thr		
165	170	175

Thr Pro Val Thr Thr Pro Pro Thr Thr Val Ala Pro Thr Thr Val Ala		
180	185	190

Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro	
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198	200	205
Ala Thr Ala Thr Pro Thr Thr Val Ala Pro Gln Pro Thr Gln Gln Pro		
210	215	220
Thr Gln Gln Pro Thr Gln Gln Met Pro Thr Gln Gln Thr Val Ala		
230	235	240
Pro Gln Thr Val Ala Pro Ala Pro Gln Pro Pro Ser Gly Gly Arg Asn		
245	250	255
Gly Ser Gly Gly Asp Ieu Phe Gly Gly Phe		
260	265	

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Ile Asn Gln Pro Leu Ala Pro Pro Ala Pro Pro Asp Pro Pro Ser Pro			
1	5	10	15
Pro Arg Pro Pro Val Pro Pro Val Pro Pro Leu Pro Pro Ser Pro Pro			
20	25	30	
Ser Pro Pro Thr Gly Trp Val Pro Arg Ala Leu Leu Pro Pro Trp Ieu			
35	40	45	
Ala Gly Thr Pro Pro Ala Pro Pro Val Pro Pro Met Ala Pro Leu Pro			
50	55	60	
Pro Ala Ala Pro Leu Pro Pro Leu Pro Pro Leu Pro Pro Leu Pro Thr			
65	70	75	80
Ser His Pro Pro Arg Pro Pro Ala Pro Pro Ala Pro Pro Ala Pro Pro			
85	90	95	
Ala Cys Pro Phe Val Pro Val Pro Pro Ala Pro Pro Leu Pro Pro Ser			
100	105	110	
Pro Pro Thr Gln Leu Pro Ala Asp Ala Ala Cys Pro Pro Ala Pro Pro			
115	120	125	
Ala Pro Pro Leu Ala Pro Pro Ser Pro Pro Ala Gly Ser Ala Ala Ile			
130	135	140	
Arg Ala Leu Thr Gly Ala Thr Ser Ala Ser Thr Leu Gly His Arg Ala			
145	150	155	160

Leu Pro Asp Asp Thr Thr Ala Arg Gly Cys Arg Arg Thr Gly
 168 170

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Gln Pro Pro Ala Glu Val Ser Asp Gln Arg Val Ser Gly Leu Thr Gly
 1 5 10 15

Ala Val Gln Pro Ser Pro Arg Thr Thr Ala Glu Asp Pro Arg Pro Arg
 20 25 30

Asn Arg Arg
 35

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Arg Ala Asp Ser Ala Gly Cys Thr Cys Arg Trp Cys Xaa Pro His Glu
 1 5 10 15

Cys Arg Arg Pro Ala Met Arg Glu Gln His Glu Ser Arg Ser Thr Thr
 20 25 30

Pro Pro Gly Pro Arg Gly Arg Ser Ala Arg Val Arg Pro Gly Arg Leu
 35 40 45

Phe Pro Trp Ala Gly Ser Ser Asp Val Phe Pro Pro Trp Phe Ala Ala
 50 55 60

Ile Met Pro Ala Arg Arg Val Gly Arg Pro Val Trp Pro Xaa Val Asp
 65 70 75 80

Gln His Thr Arg Asp Thr Gly Leu Cys Lys Leu Phe Glu Arg Arg Ala
 85 90 95

Gly Gln Leu Arg Arg Gln Phe Tyr
186

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GGATCCATAT GGCGGATCAT CATCATCATC ACGGTCAATGA CATCATCGGG ACC

53

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PCR Primer"

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

CCTGAAATTCA GGCCTCGGTT GGTGCGGCCCT CATCTTCAGAC GA

42

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PCR Primer"

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GGATCCGCA CGCTTGAAAC GACCGAGCG T

31

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

CCTTGAATTG ACCGTTGAA ATCGTCGCGA T

31

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- * (A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GGATCCAGCG CTGAGATGAA GACCGATGCC CCT

33

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GACGACATTG TCGAGAGCGG ATTTGCGCGG ACA

33

(2) INFORMATION FOR SEQ ID NO:147:

(4) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1991 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: DNA (genomic)

(v) ORIGINAL SOURCE

(A) ORGANISM: *Mycobacterium tuberculosis*

(See) FEATURES:

(A) NAME/KEY: CBS
(B) LOCATION: 152 . . 1273

(ext) SEQUENCE DESCRIPTION: SEQ ID NO:147:

TCTTCTTCGA CGGCAAGCTG TGCGGAGGAA GGCACCCACCGA ACAGCTGTTC TCTTGCGA 63

ACCATGGCGA AACGCCCGGA TACGTGCGCG GACTGTGCGG GGACGTCAGG GACGCGAGC

GGGAAATTG AAGACCAACAG AAAGCTTATGG C CTG AAA ATT CGT TTG CAT ACC 172
 Val Lys Ile Arg Leu His Thr
 | |
 S S

CTG TTG CCC GCG TTG ACC CCT CGG CGG CTG CTG CTA CGA CGG CGG CGC
Leu Leu Ala Val Leu Thr Ala Ala Pro Leu Leu Leu Leu Ala Ala Ala Gly
18 19 20

TCT GGC TCG AAA CGA CGG ACC CCT TCG CCT GAA ACG GGC GGG GGC CCC 268
 Cys Ser Lys Pro Pro Ser Gly Ser Pro Glu Thr Gly Ala Gly Ala
 15 16 17

GCT ACT GTC CGG ACT ACC CCC CGG TGG TCG CGG CTC ACC TTD CGG GAG
Gly Thr Val Ala Thr Thr Pro Ala Ser Ser Pro Val Thr Leu Ala Glu
-48 -45 -42 -39 -36 -33 -30

ACG GGT AGG AGG CTC TAC CGG CGG TTC AAC CTC TCG GGT CGG CCC
 Thr Gly Ser Thr Leu Leu Tyr Pro Leu Phe Asn Leu Trp Gly Pro Ala
 364

TTT CTC GAG AGG TAT CCG AAC GTC ACC ATC ACC CCT CAG GGC ACC GGT
Phe His Glu Arg Tyr Pro Asn Val Thr Ile Thr Ala Gln Gly Thr Gly
 35 36 37

TCT GGT GCG GGG ATC GCG CGG GCG GCG GGG ACG GTC AAC ATT GGG 460
 Ser Gly Ala Gly Ile Ala Gln Ala Ala Ala Gly Thr Val Asn Ile Gly

GCC TCC GAC GCG TAT CTG TCG GAA GGT GAT ATG GCG GCG CAC AAG GCG
Ala Ser Asp Ala Tyr Leu Ser Glu Glu Asp Met Ala Ala His Lys Gly
586

CTG ATG AAC ATC GCG CTA GCC ATC TCC CCT CGC CGC GTC AAC TAC AAC Leu Met Asn Ile Ala Leu Ala Ile Ser Ala Glu Glu Val Asn Tyr Asn 130 135 136 137 138 139	536
CTG CCC GCA CTG ACC CGC CGC CTC AAC CTG AAC GCA AAA GTC CTG CGC Leu Pro Gly Val Ser Glu His Leu Lys Leu Asn Gly Lys Val Leu Ala 140 145 146 147 148 149	604
GCC ATG TAC CGG GGC ACC ATC AAA ACC TGG GAC CGC CGC CGC ATC CCT Ala Met Tyr Glu Gly Thr Ile Lys Thr Trp Asp Asp Pro Glu Ile Ala 155 160 161 162 163 164	682
GCG CTG AAC CGC GCG ATG AAC CTG CGC CGC ACC GCA GTC GTC CGC CGC Ala Leu Asn Pro Gly Val Asn Leu Pro Gly Thr Ala Val Val Pro Leu 170 175 176 177 178 179	700
CAC CGC TCC GAC CGG TCC CCT GAC ACC TTC TTT TTC ACC CGG TAC CGT His Arg Ser Asp Gly Ser Gly Asp Thr Phe Leu Phe Thr Glu Tyr Leu 180 185 186 187 188 189	748
TCC AAC CAA GAT CGC GAG GGC TGG CGC AAG TCC CGC CGC TTC CGC ACC Ser Lys Glu Asp Pro Glu Gly Trp Gly Lys Ser Pro Gly Phe Gly Thr 200 205 206 207 208 209	786
ACC GTC CGC TTC CGC CGC CGT CGC CGT CGT CGT CGT CGC AAC CGC AAC Thr Val Asp Phe Pro Ala Val Pro Glu Glu Asn Glu Asn 220 225 226 227 228 229	844
GCC CGC ATG CTG ACC CGT TCC CGC GAG ACA CGC CGC TAC CTG CGC TAT Gly Gly Met Val Thr Glu Cys Ala Glu Thr Pro Glu Cys Val Ala Tyr 235 240 241 242 243 244	892
ATC CGC ATC AGC TTC CTC GAC CGG CGC AGT CAA CGC CGA CTC CGC CGC Ile Gly Ile Ser Phe Leu Asp Glu Ala Ser Glu Arg Gly Leu Glu Glu 250 255 256 257 258 259	940
GCC CGA CTA CGC AAT AGC TCT GGC AAT TTC TTT TTT CGC GAC CGC CGA Ala Gln Leu Glu Asn Ser Ser Glu Asn Phe Leu Leu Pro Asp Ala Gln 280 285 286 287 288 289	988
AGC ATT CGC CGC CGC CGT CGC TTC CGA TCG AAA ACC CGC CGC AAC Ser Ile Gln Ala Ala Ala Gly Phe Ala Ser Lys Thr Pro Ala Asn 290 295 296 297 298 299	1036
CGG CGG ATT TCG ATG ATC GAC CGC CGC CGC CGC GAC CGC TAC CGG ATC Gln Ala Ile Ser Met Ile Asp Gly Pro Ala Pro Asp Glu Tyr Pro Ile 300 305 306 307 308 309	1084
ATC AAC TAC GAG TAC CGC ATC GTC AAC AAC CGC CAA AAG GAC CGC CGC Ile Asn Tyr Glu Tyr Ala Ile Val Asn Asn Arg Glu Lys Asp Ala Ala 310 315 316 317 318 319	1132
ACC CGG CGC ACC TTG CGC CGA TTT CTG CGC TCG CGC ATC ACC GAC CGC Thr Ala Glu Thr Leu Glu Ala Phe Leu His Trp Ala Ile Thr Asp Glu	1180

330	335	340	
AAC AAG CCC TCG TTC CTC GAC CGG CTT CAT TTC CAG CGG CTG CGG CCC			12228
Asn Lys Ala Ser Phe Leu Asp Gln Val His Phe Gln Pro Leu Pro Pro			
345	350	355	
CGG GTC GTG AAG TTG TCT GAC GCG TTD ATC CGG ACG ATT TCC AGC			12773
Ala Val Val Lys Leu Ser Asp Ala Leu Ile Ala Thr Ile Ser Ser			
360	365	370	
TAACCTGTT GACCACCCAC CGAACGAAAC CTGGGTGCGG CGATCGGGCT GCTTTCUGA			1333
CGATGCTGC CGATGCCCGT GAATGCGGC CGCTGGGGCC CGCCATCGGC TGCTTGGTC			1393
CGATGCTGC CGCTGATCGGC CGATGCGGC CGCTGTTGAT CGTGGTGGTC CTGGTCATCG			1453
AGGCGATGCG CGGATGCGGC CGATGCGGC CGATGCGGC CGCCATCGGC GAATGGATC			1513
CGGGACAC CTACCGGAA ACCGTTGCA CGAACGGCTC CGCCATCGGC TGCGGCGCTA			1573
CTACCGGAA TTGGCGCTCA TGCGGCGAC GCTGGCGGAC CGCCATCGGC CGCGATCAT			
CGCCATCGGC CTCTCTGTCG CGCCATCGGC CGTGGTCGCG CGACCGCTGC CGAACGGCT			1633
CGCCATCGGC CGGGGAATAG CGCTGGATT CGCCCGCGA ATCCCCAGGG TGCTGCTCG			1693
TTCGCGGGG GCAATGAGCT CGCCATCGGC CGTGGTCGCG CGACCGCTGC CGAACGGCT			1753
TGCGACGGT CGCCATCGGC CGCTGCTCA CTACTGGCG CGCCATCGGC CGAACGGCT			1813
CGCCATCGGC CGCTGCTCA CGTGGTCGCG CGACCGCTGC CGAACGGCT			1873
CGCCATCGGC CGTGGTCGCG CGCCATCGGC CGTGGTCGCG CGACCGCTGC CGAACGGCT			1933
CGCCATCGGC CGTGGTCGCG CGCCATCGGC CGTGGTCGCG CGACCGCTGC CGAACGGCT			1993

(I) INFORMATION FOR SEQ ID NO:140:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(II) MOLECULE TYPE: protein

(III) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Val Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro			
1	5	10	15
Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser			
20	25	30	
Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser			
35	40	45	
Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu			

50	65	80
Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr		
65	70	75
Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala		
85	90	95
Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly		
100	105	110
Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser		
115	120	125
Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys		
130	135	140
Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr		
145	150	155
Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro		
165	170	175
Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr		
180	185	190
Phe Leu Phe Thr Gla Tyr Leu Ser Lys Gln Asp Pro Gln Gly Trp Gly		
195	200	205
Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly		
210	215	220
Ala Leu Gly Gln Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Gln		
225	230	235
Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala		
240	250	255
Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn		
260	265	270
Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Gly Phe		
275	280	285
Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro		
290	295	300
Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Gln Tyr Ala Ile Val Asn		
305	310	315
Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu		
325	330	335
His Tyr Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val		
340	345	350

His Phe Gin Pro Leu Pro Pro Ala Val Val Lys Ieu Ser Asp Ala Leu
355 360 365

Ille Ala Thie Ille Ser Ser
370

(2) INFORMATION FOR ESG ID NO:149:

(2) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

TCTTTCTTCCGA CGGCGGGGTCG CTGGGAGGAGG AGGCTCACCGA AGCGCTTTCG TCTTCCTTA 60
AGGNTGCCGA AACCGCCCCA TACGTGCGGC GACTTGGGG CGACGTTAGC GACGCCAACG 120
GCCGGAATTC AAGACCACAG AAAGCTTATGG CGTAAAATT CTTTTGATA CGCTGTTGGC 180
CGTGTTCACC GTGGGGCCGC TGCTGCTAGC AGCGCGCGGC TGTGGCTCGA AACCGCGGG 240
CGTTTCCCCT GAAGCGGGCG CGGGGGGGCG TACGTGCGG ACTTGGGGCG CGCTGTTGCC 300
CGTGACCTTG CGGAGACCG CGTGGCGCTT CGTTTACCG CGTGGCTAAC TGTGGGGTCC 360
GGCCTTTCG GAGAGGTATC CGAACGTCAC CGTGGCGCTT CGGGCGGG CGTGGCTAAC 420
CGGGTTCGG CGGGGGGGCG CGGGGGGGCG CGACGTTGG CGTGGCTAAC CGTGGCTAAC 480
GUAAGCTTGT ATGGGGGGCG AGCAAGGGCT GATGGAAACATC CGCTGACCGA TGTGGCTAAC 540
CGGGCTCAA CGTGGCGCTT CGGGGGGGCG CGACGACCTC AGCTGAACT CGAAAGCTTG 600
GGGGGGGGCG TACGGGGCG CGATGAAAC CGTGGACGNC CGGGGGGGCG CGTGGCTAAC 660
CGGGGGGGCG AGCTGGGGCG CGACGCGGGT AGTTGGGGCG CGGGGGGGCG CGGGGGGGCG 720
TGACGACCTC TTGTTGACCC AGTACCTTCG CGAGCAAGAT CGGGGGGGCG CGGGGGGGCG 780
GGGGGGGGCG CGGGGGGGCG TGGACTTCCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG 840
CAACGGGGCG ATGGTGGCG CGTGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG 900
CGGGGGGGCG GACGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG 960
TGGGGGGGGCG AGCGGGAAAG CGTGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG 1020
GAAAGGGGGCG CGGGGGGGCG CGATTTGGAT GATGGGGGGCG CGGGGGGGCG CGGGGGGGCG 1080
GATGATGAAAC TACGAGTACG CGATGTTCAA CAACGGGGCG AGGGGGGGCG CGGGGGGGCG 1140

100

GACCTTCAG GCAATTGTC ACTGGCGAT CACCGACGCC AACRAGGGCTT	1200
CCAGGTTCAT TTGAGCGGC TCCCGCCCGC CCTGGTGAAAG TTGTCTGAGG CTTGGATGCC	1260
GACGATTTGC AGCTAAGCTC GTTGACCCAC ACCGGACACSC AACCTCCCTC CGGGCTGCG	1320
CTCTCTTTGC GGAGCATGT GGGCGTCCC CCTGAGCTGC CGCGCTGCG CGGGCGCTGC	1380
CGGTGGTTGC CTGGGATGG TGCGGTGATC CGCGCTGCG CGCTGGCTTT CGCTGCGTGC	1440
CGCTGGCTCA TCGGGCGAT CGGTGGCGTC AGGGTCAACG CGTGGCGTTT CTTCAGCGCC	1500
ACTGGATGGA ATGGAGGCGA CACCTGGTC GAAACCGTTC TCACCGACCC CGGGCGCTGC	1560
CGGTGGCGC CTACTGGCG CGGTGGCTGC TGATGCGTG CGCGTGGCG ACCTGGCGA	1620
TGACCGTGT CATGGCGGTG CGGTGGCTGC TAGGAGCGGC CGCTGGTATC CGGGACCGC	1680
TGCTGAAACG CGTGGCGCG CGCTGGCGAA TGTCTGCGA ATTGTGCGC GGAATGGCGA	1740
CGCTGGCTGC CGGTTTGCG CGGGCGATCA CGTGGCGCC CGCTGGCTGC CGTGGACATG	1800
CTGGCGTGT CGCTGACAAAC CGTGGCGATCG CGCTGGCTGC GAACTACTTC CGCGGGCGCC	1860
CGGGCGACCG CGGGCGATG TTGGCTGCG CGCTGGCTGC CGGGCGATG CGCTGGCGCA	1920
TTATGGCGAC CGGGCGAT CGCTGGCTGC CGGGCGATG CGTGGCGCC CGGGCGACCG	1980
CGATGGCGAA TTC	1993

(B) INFORMATION FOR SEQ ID NO:150.

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids.
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150.

Met Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro			
1	5	10	15

Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser			
20	25	30	

Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser			
35	40	45	

Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu			
50	55	60	

Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr			
65	70	75	80

Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
 85 90 95

Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
 100 105 110

Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
 115 120 125

Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
 130 135 140

Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr
 145 150 155 160

Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
 165 170 175

Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
 180 185 190

Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
 195 200 205

Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
 210 215 220

Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Gln
 225 230 235 240

Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
 245 250 255 260

Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
 265 270 275 280

Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Gly Phe
 275 280 285

Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
 290 295 300

Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 305 310 315 320

Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 325 330 335

His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 340 345 350

His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 355 360 365

Ile Ala Thr Ile Ser Ser

370

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GGTCTTGACC ACCAACCTCGG TGTCCGAAGTC GGTACCGGAA TTGAAGTCCA GGTACTCTG	60
GCTGGGGCGG CGCAAACAAAT AGCCGACAAGC ATTCGAAACAG CGCCGGTAGC CTTTGACGCT	120
GTAGCCAAAC CGCAACGCCG CGCGCTTGG CACCTTTTCG AGCGCTTATT TGACACAAAC	180
CTGGTGGAG CTGATGCCGT CGAATTGTTGC CGGGCGAACG CTGGGGGCCA CGCCGATCCG	240
CTGCAACCGG CGAEGGCCG TGTCGAACG GGTGCGGTT CGCCGAGACG GGTGCGGCG	300
CGCAACGCGT ACCATTATTC GAACAAACGT TGTATACTTT GTGAACTTTC CGCGCTTACG	360
AGCGCTTCAC AGGATGTTAT ATGCCATATTC TGCGCGACA CGACGGAGCC AGCGCTTATG	420
ACGCGATTTC CGTCCGACCC CTACGGCGAC CGCGACTTACG TAGAAATTGC CGCGAACCGC	480
ATGGCGTATA TGACGGAAAGG CAACGGTACG CGCATCGCTT TTGACCGCGG CAACGGCGAC	540
TGTTTACT TGTEGGCGCA CGTCATGGCG CACTTGGAGG CGCTGGGGCG GGTGGTGGCC	600
TGGCGATGTA TGCGGATGGG CGCGTGGAC AGGCTGAACCC CGTGGCGACCG CGCGCGTAT	660
AGCTTATGCC ACCAACCGAGA CTTTTTTTTC CGCTCTCGG ATGGCTCTGA CCTCGCGCAC	720
CGCGTGTAC TGCTGCTTCA CGACTTGGCG TGCGCGCTCG GCTTGGACTG CGTAAACCG	780
CGTCCGGACC GACTGGCGGG GATGGAACTCA TGCGAACTCA TGTCACCCC GATGACTTGC	840
CGCGACTTGC CGCGGGCGGT CGCGGGTGTG TTCAGGGTT TCCGATGGCC TGACGGCG	900
CGTATGGCGT TGAGGCACAA CGTCCTTGTG CGACCGTACG TGCCCCGGGC CGTGGCGCA	960
CGCTCGACCG ACCAGGAAT GAACCGTAT CGCGCGCCAT CGGTGAACCG CGCGAGGAC	1020
CGTACGTTCA CGTTCGTCG CGCACGAAAC CTTCCAAATCG ACGCGTGGACCC CGCGAGGTC	1080
CTGCGTTGG TGTACGGAGTA CGCGAGCTCG CGACGATGCC CGAAGCTTTC	1140
ATGAAACGGCG AGCGCGCGCG GATGATGCC CGCGCGATCC GTGACTTATGT CGGAGCTCG	1200
CGCAACCGAGA CGCGAATCAC AGTGGCCGGC GTGGCTTTCG TTCAGGGAGCA CGCGGATGCG	1260
CGCGTATCGT CGCGGGCGTC CGCGGCGCGT CGCGGCGCTG CGTGGCGCA	1320

GACCAAGAAT	GTGTTTGC	CCCAAGGCG	CCCCCTGCTT	GTCAACTCAT	AAGACTTCT	1380
GTCCCGGCA	GAGATTTCGA	GGAAAAAGGG	CACCAATGCC	ACCCGCTTCC	TTCGCGAACGGA	1440
GTCAGACAAA	TATACGTCGC	AGGACAAAGG	TCTTCTTATT	TGCCCCGGGA	ATTAGTCCT	1500
CCCTTCTAT	GGCTCACTT	CGAGGAAGCC	GAACCGATCA	CCCTATCGG	ATTGGACCTA	1560
TGAAACGCT	ATCTGAAAG	CTTCCAATCA	TTGGAACGCC	CCGGCTCTCT	CCGCCCTCCC	1620
ATCATCCAC	AGGGCTGCTC	TCAGAACGCC	CAAGTGACT	ACGTOTTACT	ACGCCCGAGC	1680
CCGATGGG	AGGAGTCTT	GGCCGTTTG	ACAGAGCAG	GTATAGCCG	GTCTTTCT	1740
TACCTCCGC	TTCACGGATTC	CCCGGCCCGG	CTTCCT			1777

(2) INFORMATION FOR SEQ ID NO:152:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GAGATTGAA	CTTACCGCTC	TCTTACGCCG	CTCCCTCCCG	TGAATGCCCA	TATCAACGAC	60
GGCCATUTTC	TGCTTGTGCA	CTTTTGCGCC	ATGCCCCGAC	CTTGCTTAAAC	CGGGCTTTC	120
ATCAGTAAATT	CGGTTTACCC	CTTGCGCGAA	CCGGCGGAGG	ATGTCGTTTA	CCGGCGGCG	180
CCACCATCCC	CGACGAACTC	CTGGATGCTC	AGGGCGGCTG	CGGGCACTTA	CCGAGCTTT	240
CCGGCGGATG	CTCCGACTG	CTACTCGGCT	GGGGCGGCTG	CCGGCGGCTT	CGCTGAAGAC	300
CGTGACCCGAC	CCGGCGGATT	CGAGCGCGG	CCGGCGGCTT	CGCTGAAGAC		324

(2) INFORMATION FOR SEQ ID NO:153:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GGCGTACCGG	CCCGTTTGGC	TGGCACGGGA	CTCTGACGAC	CTGAAACGCT	TGGCTCGCG	60
AAGGATTCAC	GAACCGCTCG	TGCGCGGCT	CTGGCTGCTC	AAGGTGTCGG	CTGATGTCGT	120
CGATGACCGG	CCGGCGGCTT	GGCGCTACCG	CTCTGAGAC	CTGCTCGCGG	CCCGCGGCGA	180

GCACCCATTC CAGCCCCACT CAATGGGCTT CCTAACCTTT CCTTGTGCTTA TGGCTGCTT
CGAAGCTTCC GTCGCGAACC GATTTGCCCTT CCTCACTTAC CTCAGCCCG ACCAGCGCG
CTGGCCGCCG TGGAGGAAAC GCCTCCGCCG CGAAGTGGAG ACGCGCTTCC CGCTTGCG
CTTCTTGTCA ACCTTCGGGC GATGCTGCCS TTCTGGCTGCC AGGGTTGCCG CTGGACCCCG
CTGAATCCAC TAGATGAGAC CAGTTGCCCA CGAATCCGGC TGTGGTGGT AGCGAGACAC
GAGTACTTTC ATGAGTATTG GATGCACTTG ATGACCCGGC TGATTCAAGCA CGACCAATCG
AACTGGCCCG CGCAAAACGT CTCUGAGATG ATCGGCGTCC CCTTGAACC CTGGCTTCT
GGCTCATTC CGACATTTT CGGCTTCCC GATTTCTCTT CGCCGAGCG CTGAAGCT
CGAAGCCGGC CGTGACCCG CTGCTGGAC CGGGCGAGC CGCTCTCTG CGTAACCCCG
CGATTCGGCA GAAAGGTTTC GAGGTGGCG CGCAAGCTTTT CTGTTTTCG CGGACCGTG
CGCACAGCCA CGGGAGCCG GTTGGCCCG AGCAACCGCA CCTGGTGGCG CGGGCGCCCG
CGACACAC CGACGACTT GTGCTACTTG CGGGCGAGC CGAAGTTTTT CGGGCGCTTG
CGTTAACCG CGACGACTT CTGCAACCGCA TGAGGATCT CGACATCTTG ACCGGCGCT
CGCTGGCGGC CGAGCGCTTC GACTTTCGGC CGAACACAA ACTGGCTTC TTGGCTGTCT
CGGGATTCG CCTGGCCGAG CGGGTGGCG TGCGGCTTG CGGGGACTAC CGGGCGTCA
CGACGACTT CGACGACCG AGTGGCCCGA CCTGGGGCC CGGGTGGAC CGGGGGCG
CGCTGGCCG CCTGGCCGAG CGGGTGGCG AGGGCTGGG TTGGCTTGCG CGACATCTTG
CGGGTGGAC TGTACGCCCA CTGGGGCTTG CGAGTGTCTT CGGGTGGCTT CGGGGGCG
TGGGGTCAAT TGACGCCCG CGAACACCGA CGATGGCCG CGGGTGGTC CGGGGGCG
CGGGGGCG CGACGACCG

(2) INFORMATION FOR SEQ ID NO:154:

4.2 SEQUENCE CHARACTERISTICS

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

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CCGGCGGAC CGGGTGACC GCGGTACCG GCGGCGACCG CCTTGAGCCC GCTGCTGCG 60
TGGGCTTCG CGCGAACGC GACCGTGTG TGGCTGGCG CAAAGCGGT AACGGCGAA 120
TAGGTGGGC CGCGTGACA GCGGGTGGC GCGGGCAAGC GCGGAGGCG GCGGAGGCG 180

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GCACCGGCGG TTTGGGGCGC CCTTGGCAACG ACCGGGGGGG CACGGGCGAT CGGGGGCGTA	340
AAGGGCGGGAA CGGGGGGATTC CGCGGTGCCG CGGGGGGGGG CGGGGGGGCC CGGGGGGGAA	360
ACGGGCGGGCA TGGGGGGAAC C	381

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GAAGGACGGG CGGGGGGAA TCGATGGCT CGGGGGACTAC TTTGGGGCGA CGGGGGCGTG	60
CGGGGGCGG CCTGGGGGGTC AGCGGGGGCT ACGGGGGGAA CGGGGGGGAA TGCGGGGGCG	120
CGGGGGGGG CGGGGGGGTC CGGGGGGGTC ACTGGGGGGG GAGGGGGGGG CGGGGGGGGG ATCGGGGGGG	180
CGGGGGGGGG CGGGGGGGCA AAGGGGGGGG TGCGGGGGGG CGGGGGGGGG CGGGGGGGCT	240
ACGGGGGGCT CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG GATGGGGGGG TTTGGGGGGG	300
GAGGGGGGGG CGGGGGGGGG GTGGGGGGGG CGGGGGGGGG TTTGGGGGGGG CGGGGGGGGG	360
TGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG	420
ATGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG	480
ACGGGGGGGG CGGGGGGGGG GT	492

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Ser Ala Glu His Leu Val Glu Gly Asp Ala Val Glu Leu Trp Arg Ala			
3	5	10	15
Asn Ala Ala Asp Glu Ala Asp Pro Leu Gln Pro Gly Ser Ala Arg Arg			
20	25	30	
Gln Arg Ala Ser Arg Ser Pro Arg Arg Leu Ala Gly Pro Asn Ala Tyr			
35	40	45	
His Tyr Ser Asn Asn Arg Ser Ile Leu Cys Glu Arg Trp Pro Leu Pro			

80

55

60

Ser Ala Ala Gln Asp Val Ile Cys His Leu Cys Pro His Arg Gln Glu
 65 70 75 80

Pro Gly Leu Met Thr Ala Phe Gly Val Glu Pro Tyr Gly Gln Pro Lys
 85 90 95

Tyr Leu Glu Ile Ala Gly Lys Arg Met Ala Tyr Ile Asp Glu Gly Lys
 100 105 110

Gly Asp Ala Ile Val Phe Gln His Gly Asn Pro Thr Ser Ser Tyr Leu
 115 120 125

Trp Arg Asn Ile Met Pro His Leu Glu Gly Leu Gly Arg Leu Val Ala
 130 135 140

Cys Asp Leu Ile Gly Met Gly Ala Ser Asp Lys Leu Ser Pro Ser Gly
 145 150 155 160

Pro Asp Arg Tyr Ser Tyr Gly Glu Gln Arg Asp Phe Leu Phe Ala Leu
 165 170 175

Trp Asp Ala Leu Asp Leu Gly Asp His Val Val Leu Val Leu His Asp
 180 185 190

Trp Gly Ser Ala Leu Gly Phe Asp Trp Ala Asn Gln His Arg Asp Arg
 195 200 205

Val Gln Gly Ile Ala Phe Met Glu Ala Ile Val Thr Pro Met Thr Trp
 210 215 220

Ala Asp Trp Pro Pro Ala Val Arg Gly Val Phe Gln Gly Phe Arg Ser
 225 230 235 240

Pro Gln Gly Glu Pro Met Ala Leu Glu His Asn Ile Phe Val Glu Arg
 245 250 255

Val Leu Pro Gly Ala Ile Leu Arg Gln Leu Ser Asp Glu Glu Met Asn
 260 265 270

His Tyr Arg Arg Pro Phe Val Asn Gly Gly Glu Asp Arg Arg Pro Thr
 275 280 285

Leu Ser Trp Pro Arg Asn Leu Pro Ile Asp Gly Glu Pro Ala Glu Val
 290 295 300

Val Ala Leu Val Asn Glu Tyr Arg Ser Trp Leu Glu Glu Thr Asp Met
 305 310 315 320

Pro Lys Leu Phe Ile Asn Ala Gln Pro Gly Ala Ile Ile Thr Gly Arg
 325 330 335

Ile Arg Asp Tyr Val Arg Ser Trp Pro Asn Gln Thr Glu Ile Thr Val
 340 345 350

Pro Gly Val His Phe Val Glu Asp Ser Asp Gly Val Val Ser Trp
 365 360 365
 Ala Gly Ala Arg Gln His Arg Arg Pro Gly Ser Ala Leu Ile Ser Arg
 370 375 380
 Asp Gln Glu Cys Asp Phe Arg Arg Arg Arg Pro Ala Cys Gln Leu
 385 390 395 400
 Ile Arg Leu Pro Ala Pro Gly Arg Asp Ser Gln Gly Lys Gly His Gln
 405 410 415
 Ser Gln Pro Leu Pro Ser Gln Arg Gly Arg Gln Ile Tyr Val Ala Gly
 420 425 430
 Gln Arg Ser Ser Tyr Leu Pro Ser Glu Leu Val Ala Ala Phe Leu Trp
 435 440 445
 Ala Gln Phe Glu Glu Ala Glu Arg Ile Thr Arg Ile Arg Leu Asp Leu
 450 455 460
 Trp Asn Arg Tyr His Gln Ser Phe Glu Ser Leu Gln Arg Gly Leu
 465 470 475 480
 Leu Arg Arg Pro Ile Ile Pro Gln Gly Cys Ser His Asn Ala His Met
 485 490 495
 Tyr Tyr Val Leu Leu Ala Pro Ser Ala Asp Arg Glu Glu Val Leu Ala
 500 505 510
 Arg Leu Thr Ser Gln Gly Ile Gly Ala Val Phe His Tyr Val Pro Leu
 515 520 525
 His Asp Ser Pro Ala Gly Arg Arg
 530 535

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: Linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Asn Glu Ser Ala Pro Arg Ser Pro Met Leu Pro Ser Ala Arg Pro Arg		
1	8	16
Tyr Asp Ala Ile Ala Val Leu Leu Asn Glu Met His Ala Gly His Cys		
20	28	36
Asp Phe Gly Leu Val Gly Pro Ala Pro Asp Ile Val Thr Asp Ala Ala		
38	46	48

Gly Asp Asp Arg Ala Gly Leu Gly Val Asp Glu Gln Phe Arg His Val
 50 55 60

Gly Phe Leu Glu Pro Ala Pro Val Leu Val Asp Gln Arg Asp Asp Leu
 65 70 75 80

Gly Gly Leu Thr Val Asp Trp Lys Val Ser Trp Pro Arg Gln Arg Gly
 85 90 95

Ala Thr Val Leu Ala Ala Val His Glu Trp Pro Pro Ile Val Val His
 100 105 110

Phe Leu Val Ala Glu Leu Ser Gln Asp Arg Pro Gly Gln His Pro Phe
 115 120 125

Asp Lys Asp Val Val Leu Gln Arg His Trp Leu Ala Leu Arg Arg Ser
 130 135 140

Glu Thr Leu Glu His Thr Pro His Gly Arg Arg Pro Val Arg Pro Arg
 145 150 155 160

His Arg Gly Asp Asp Arg Phe His Glu Arg Asp Pro Leu His Ser Val
 165 170 175

Ala Met Leu Val Ser Pro Val Glu Ala Glu Arg Arg Ala Pro Val Val
 180 185 190

Gln His Glu Tyr His Val Val Ala Glu Val Glu Arg Ile Pro Glu Arg
 195 200 205

Glu Glu Lys Val Ser Leu Leu Ala Ile Ala Ile Val Gly Ser Arg
 210 215 220

Trp Ala Glu Leu Val Arg Arg Ala His Pro Asp Gln Ile Ala Gly His
 225 230 235 240

Gln Pro Ala Glu Pro Phe Gln Val Arg His Asp Val Ala Pro Gln Val
 245 250 255

Arg Arg Arg Gly Val Ala Val Leu Lys Asp Asp Gly Val Thr Leu Ala
 260 265 270

Phe Val Asp Ile Arg His Ala Leu Pro Gly Asp Phe
 275 280

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ATGAAACATGT CCTCGGGGGT CGGTCGGAG GCCTTGCGC GATTCGGGG CTACTCTCC	60
GCCATGCACG CGATCGGGG TTTCTCGAT GCGTTGCCCT AAGAGCTGGG GGUTAAGGAA	120
ATCCCCCTCT CGTCAATCAA CCCGGCTG ACCCACACAC CGCTTGGC CAACCTGGAC	180
CGGGCGACA TGGCGCGCTT GTTTCCGAGC CTCACCGCCA TTGGCGTCA CTGGGGCGG	240
CGACCGCTGC TTGACCGCTG AGCG	264

(3) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

TAGTCGGCGA CGATGACGTC CGCGTCCAGG CGAACCGGTT CAASCACAG CGUGACCCAG	60
AAGCCGCTGC GATCCCTTACG CGCGAAGCAG TGCGTCAACG CGGGCGCTCC CGGGCGAAGC	120
ACGTCGACCA CGACATGATAC CGCGCGCTGT CGTCGATTTC CGGTTGGAA TTGGCGATAC	180
TCGGCGTCA TGTCACCGCTT CGACCGCTCA TTTCATCGACT CGCTTGATTG CGCGACGTC	240
CGGTTGACC CGTCATTTGT TAGCAACCTC TTGAATGCCG TTTCGGCGCG CGCTGACGTC	300
TCGGCGCTTG CGCGCGGAG CGCGCGAAC CGCGCGCGCT CGACCGCGAT CGCGCGCGAA	360
ACCGCGCTCG CGCGCGCGCG CGCAACCTCG CGCGCGCGCC CGACCGCGTC AACGGCGCGTC	420
ATGTCGACCG CGCGCGCGCT CGCGCGCTCG CGACCGCGCT CGCGCGCGAC	480
CGACCGCGAC CGACCGCGAC TTGCGCGCTA CGGATCGTC CTTCGGCGTC CGCGCGACCA	540
ACGTCGATCG CGCGCGCGCT CGATCGCTTC ACAGACGACG CGCGCGCTGT	600
CGCGCGCTGT ATGTCGACCG CGACCGCGCT CGACCGCGTC CGCGCGCGCG	660
ACGTCGACCG CGACCGCGCG CGCGCGCGCT CGACCGCGCT CGCGCGCGAC	720
CGCGCGCTAA CGCGCGCGCG CGCGCGCGCG CGACCGCGCG CGCGCGCGCG	780
CGCGCGCGCT CGTGGCGGTT CGTCGACCGC TTTCGGCGCT CGCGCGCGCG CGCGCGCGCG	840
TTATCGACCT CGCGCGCGCG CGACCGCGAC CGCGCGCGCT CGTCGACCGT CGACGACGTC	900
ACGTCGACCG CGACCGCGCG CGCGCGCGCG CGACCGCGCG CGACCGCGCG	960
CGACGACGTC ACATCGCGCG CGCGCGCGCG TTTCGGCGCT CGACGACGTC CGCGCGCGCG	1020

CCGACCCCGG TGTGTTCCCA CCTACGCCAC CGCTCCGACA CCAGTTTGT GCCCCCACTA	1088
ACCATGGCGG ACCTCCGCTA TACCGGGCT CGCACAGCTG TCCCGAAAGA TGTCCGGCG	1140
GGGGCGCTTG CAGTCCTGGC CGTTCCGCAA C	1171

(ii) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

CCAAAGGGCG CAGGGGGCG CGCCGATGA ACGACCTCGA CGCGCTGTA CGGGCCGAG	60
ACGGCGGCGA ATGGGGCGAC CGCGGCGG CGCGGAAACGC CGCGGGCGC CGCACCGCT	120
TGACCCGAGG CGCGGACGGC AACGGGGCGA AGCGCGTGA CGCGGGGTC CGGGCGAAG	180
CGGGAAACCG CGGAAACGGC CGAGACGACA CGACGACCGC CGGGCG	227

(ii) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

CGTCCGCAAC ATGGGGCGGGC AGGGCGCTAG CGTTCGCGCC GCGTTAACCC CGGGCGGCAA	60
GGGGCGGCGAC CGTTTACTC CAACCGAGCG CGGGGACGCG CGGGCGCGCG CGAACGGCGCG	120
CGACTCCAA CGGGCGCGCG CGAACGGCG CGGGCGCGCG AATGGGGCGA AGGGCGCGAG	180
CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG	240
CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG	300
CGGGCGCGCG	364

(ii) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

CTGGGACCT	CCCGAGGTC	TATAACAAG	AACAACTGCA	CCAGGCGCCG	CTTGTTTACG	60
TCATCGACCT	ATTAAACCT	GCGGCTTCG	GCCTGCCAGG	CGAGGCACCGC	GGCGCGATC	120
TGATGCTTA	GGTCTACAA	TACTTCTG	CCAATTTCG	TGGACGCAA	GGAAACCGG	180
GTGGGACCT	CTTTACCCG	CGCGCTTG	TCAAGCTCAT	CCTGGACCT	CTGGGACCT	240
CGAATGCGG	CGTGTATGAC	CCCTGCTCG	GTTCCCGAG	CATTTTGTG	CACACCCGA	300
AGTTCACTTA	CGAACACAC	CGCGATGGA	AGGATGTC	CATCTATGGC	CGGGAAAGCA	360
TTGAGGAGAC	CTGGGCGT	CGCAAGCTGA	ACCTGGGCT	CCACGGGTC	CACACGAGG	420
GGCTGGCG	CGCGATGGCT	GTTCCTTG	CCCGCGAC	CGACCGGAC	CTGGGAGATG	480
ACTTACCTAT	CGCGATGCG	CGCTTACAA	TCAAGACTG	CCCGCGAAC	CACGAGACG	540
CGCGCTGGG	CTTGGGTTT	CCCGCGGCG	ATTAACCGAA	CTACCGATG	ATTGNGGCA	600
TCCTGATCA	CTTGGGCGG	CGACGCGCG	CGCGCTGTT	GATGGCCAA	GGGTGATGT	660
CCTGGAACTC	CGACGGGCG	ACCGCTGTT	TCCCGACAC	CGGAACTCG	CTGGGCGTGT	720
CGTTTTGCG	GAAGACGAG	ACCGATGTC	TATCAACCG	TGCGGCGG	ATTTGGTTT	780
TGCTGTTTGT	CGACGGCTG	ACCTGGCT	ACCGGGGAC	CGGGGAAAT	CGTGGAGCG	840
CGACGGGCG	CGCGATGTC	ACCGCTGTT	TCCCGACAC	CGGAACTCG	CTGGGCGTGT	900
CGACGGGCG	CGACGGGCG	ACCGCTGTT	TCCCGACAC	CGGAACTCG	CTGGGCGTGT	960
CGCGCTGGG	TGTTGGGCG	CGTAAATGGG	CGACGGCT	CGACGGGCG	CGCGCTGTT	1020
CGCGCTGGG	CGACGGGCG	CGTAAATGGG	CGACGGCT	CGACGGGCG	CGCGCTGTT	1080
ACCGGGCGAA	CGCGGGGAC	CGCGGGGAC	ACCGGGGAC	CGACGGGCG	CGCGGGGCG	1140
CGAAACGGG	CGACGGGCG	ACCGGGGAC	CGACGGGCG	ACCGGGGAC	CGACGGGCG	1200
CGCGGGGCG	CGACGGGCG	CGACGGGCG	CGACGGGCG	CGACGGGCG	CGCGGGGCG	1260
CGCGGGGCG	CGACGGGCG	CGACGGGCG	CGACGGGCG	CGACGGGCG	CGCGGGGCG	1320
CGCGGGGCG	CGACGGGCG	CGACGGGCG	CGACGGGCG	CGACGGGCG	CGCGGGGCG	1380
TCAACTCAC	CGCGGGGCG	CGACGGGCG	CGACGGGCG	CGACGGGCG	CGCGGGGCG	1440

(2) INFORMATION FOR SEQ ID NO:163:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single